

GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 14, 2003, 09:06:48 ; Search time 36 Seconds  
(without alignments)  
70.327 Million cell updates/sec

Title: US-09-359-426C-2

Perfect score: 81  
Sequence: 1 XEKKPLTTAXAPVXNA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

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Prdcd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	93.8	19	19	AAW64480
2	76	93.8	19	22	AAW64480
3	44	54.3	291	21	AAW64480
4	44	54.3	292	21	AAW64480
5	44	54.3	306	22	AAW64480
6	44	54.3	306	22	AAW64480
7	44	54.3	427	21	AAW64480
8	42	51.9	172	21	AAW64480
9	42	51.9	215	21	AAW64480
10	42	51.9	332	21	AAW64480

11	41	50.6	1012	22	ABB66926
12	40	49.4	258	23	ABB48482
13	40	49.4	445	22	AAU36108
14	40	49.4	498	15	AAW51691
15	40	49.4	498	20	AAW93076
16	40	49.4	788	22	ABB65083
17	40	49.4	1473	22	ABB68024
18	39.5	48.8	1793	22	ABB59613
19	39	48.1	128	21	AAW36990
20	39	48.1	137	22	ABB26339
21	39	48.1	233	22	AAW91909
22	39	48.1	321	23	AAE22281
23	39	48.1	395	23	AAE22282
24	39	48.1	395	23	AAE22283
25	38.5	47.5	842	22	ABB67966
26	38	46.9	225	22	ABB71511
27	38	46.9	229	22	ABB94775
28	38	46.9	229	22	ABB81876
29	38	46.9	229	23	AAU81227
30	38	46.9	261	22	AAW91455
31	38	46.9	277	22	AAU18229
32	38	46.9	307	11	AAW07361
33	38	46.9	521	15	AAW63672
34	37	45.7	19	22	AAU27612
35	37	45.7	120	21	AAW18092
36	37	45.7	123	22	AAW05456
37	37	45.7	326	22	AAW93916
38	37	45.7	358	22	ABG01028
39	37	45.7	396	23	ABP28665
40	37	45.7	440	22	ABG01280
41	37	45.7	456	21	AAW54289
42	37	45.7	498	18	AAW06454
43	37	45.7	500	21	AAW54314
44	37	45.7	500	21	AAW54314
45	37	45.7	500	21	AAW54315

## ALIGNMENTS

RESULT 1	AAW64480	standard; peptide: 19 AA.
ID	AAW64480	
XX	AAW64480	
AC	AAW64480	
XX	AAW64480	
XX	20-OCT-1998	(first entry)
DE	P. aeruginosa protein antigen Pa60 N-terminal peptide fragment.	
XX	Antigen: Pa60; diagnosis; detection; cystic fibrosis; vaccine;	
KW	Immunogen; infection; treatment.	
XX		
OS	Pseudomonas aeruginosa.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 1	/label= unknown
FT	Misc-difference 12	/label= unknown
FT	Misc-difference 17	/label= unknown
FT	Misc-difference 17	/label= unknown
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PN	W09832769-A1.	
XX		
PD	30-JUL-1998.	
XX		
PF	26-JAN-1998.	98WO-GB00217.
XX		
PR	24-JAN-1997.	97GB-0001489.
XX		
PA	(AUSP-) AUSPHARM INT LTD.	
	(CHAP/) CHAPMAN P W.	

Drosophila melanog  
Listeria monocytog  
Klebsiella pneumon  
HIV-type virus MWP  
HIV isolate 5180 g  
Drosophila melanog  
Drosophila melanog  
Drosophila melanog  
Arabidopsis thalia  
Novel human diagno  
C glutaric prote  
Murine SPAS-1 part  
Murine tumour SPAS  
Murine normal SPAS  
Drosophila melanog  
Drosophila melanog  
Human protein sequ  
Double strand RNA  
Human Lung cancer  
C glutaric prote  
Novel human DNA-bi  
Phospholipase D to  
Aldehyde-dehydroge  
Human LEXRI protei  
Arabidopsis thalia  
Human polypeptide,  
Novel human diagno  
Streptococcus poly  
Novel human diagno  
Consensus sequenc  
Capsicum annuum ly  
Amino acid sequenc  
Amino acid sequenc  
Amino acid sequenc

XX		Clancy RL,	Cripps AM,	Dunkley M,	Kyd J;
PI		WPI; 1998-427879/36.			
XX					
DR					
XX					
XX					
PT		Protein antigen from Pseudomonas aeruginosa and its antigenic fragments - useful diagnostically to detect specific antibodies, particularly in patients with cystic fibrosis, and as vaccines			
XX					
PS		Claim 3; Page 2; 23pp; English.			
CC					
XX		This peptide is the N-terminal fragment of a novel Pseudomonas aeruginosa protein antigen, Pa60. This fragment could be used for diagnostic detection of P. aeruginosa by forming complexes with specific antibodies, particularly in patients with cystic fibrosis (by analysis of mucus, e.g. in saliva), or in vaccines or immunogenic compositions to treat or prevent infection by P. aeruginosa.			
CC					
CC					
CC					
CC					
CC					
SO		Sequence 19 AA:			
Query Match		Best Local Similarity 93.8%; Score 76; DB 19; Length 19;			
Matches 18; Conservative		100.0%; Pred. No. 3.1e-06; Mismatches 0; Indels 0; Gaps 0			
OY		2 EEKTPLTAAAXAPVYXNA 19   Db 2 EEKTPLTAAAXAPVYXNA 19			
RESULT 2					
AAB69062					
ID		AAB69062 standard; peptide; 19 AA.			
AC					
XX		AAB69062;			
XX					
DT		18-APR-2001 (first entry)			
DE		Pseudomonas aeruginosa protein N-terminal peptide.			
XX					
XX		Pseudomonas aeruginosa; chitinase; groEL; chiA; antigen; vaccine;			
KW		diagnosis; detection; infection; immune response.			
XX					
OS		Pseudomonas aeruginosa.			
XX					
FH		Key Location/Qualifiers			
FT		Misc-difference 1 /note= "unspecified"			
FT		Misc-difference 12 /note= "unspecified"			
PT		Misc-difference 17 /note= "unspecified"			
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XX		WO200102577-A1.			
PN					
XX					
XX		11-JAN-2001.			
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XX					
PF		03-JUL-2000; 2000WO-GB02554.			
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PR		01-JUL-1999; 99GB-0015419.			
XX		(PROV-) PROVALIS UK LTD.			
PA					
XX					
XX					
PI		Smith CJ, Thompson SE, Smith MW, Peek K, Sizer PJH, Wilkinson MC;			
PI		WPI; 2001-080988/09.			
DR					
XX					
PT		Antigenic Pseudomonas aeruginosa proteins, useful in the detection and/or diagnosis of P. aeruginosa infections and for producing vaccines against P. aeruginosa -			
XX					
XX					
PS		Disclosure; Page 2; 129pp; English.			
XX					
CC		The present invention describes antigenic Pseudomonas aeruginosa			

CC	proteins/P1). The P. aeruginosa proteins have antibacterial activity				
CC	and can be used in vaccines and as antagonists. The proteins or their				
CC	fragments, or antibodies are useful in the detection and/or diagnosis				
CC	of P. aeruginosa. They are also useful for producing a vaccine and				
CC	including an immune response against P. aeruginosa infection. An agent				
CC	capable of antagonising, inhibiting or otherwise interfering with the				
CC	function or expression of p1 are useful in the manufacture of a				
CC	medicament for the treatment or prophylaxis of P. aeruginosa infections.				
CC	The present sequence represents a probable P. aeruginosa protein				
CC	N-terminal peptide sequence from the present invention.				
XX					
SQ	Sequence 19 AA:				
 Query Match 93.8%; Score 76; DB 22; Length 19;					
Best Local Similarity 100.0%; Pred. No. 3;le-06;					
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	2 EEKTPLTAAAXAPVYXNA 19 				
Db	2 EEKTPLTAAAXAPVYXNA 19				
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ID	AAG30091 standard; Protein; 291 AA.				
AC	AAG30091;				
DT	17-OCT-2000 (first entry)				
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 35912.				
XX					
MW	Protein identification; signal transduction pathway; metabolic pathway;				
KM	hybridisation assay; genetic mapping; gene expression control; promoter;				
XX	termination sequence.				
OS	Arabidopsis thaliana.				
FN	EP1033405-A2.				
PD	06-SEP-2000.				
PF	25-FEB-2000; 2000EP-0301439.				
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PR	25-FEB-1999; 99US-0121825.				
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PR	09-MAR-1999; 99US-0123548.				
PR	23-MAR-1999; 99US-0125788.				
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PR	01-APR-1999; 99US-0127462.				
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PR	08-APR-1999; 99US-0128714.				
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PR	19-APR-1999; 99US-0130077.				
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PR	28-APR-1999; 99US-0131449.				
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Query Match 54.3%; Score 44; DB 21; Length 291;  
Best Local Similarity 60.0%; Pred. No. 17;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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RESULT 4  
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ID AAG30090 standard; Protein; 292 AA.  
XX AAG30090;  
DE 17-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 35911.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35911.  
XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX Arabidopsis thaliana.  
XX EP1033405-A2.  
XX 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
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DE	Amino acid sequence of a deoxyribokinase enzyme.			
KW	Deoxyribonucleoside; deoxyribose 1-phosphate; thymidine phosphorylase;			
KW	purine nucleoside phosphorylase; phosphopentose mutase;			
KW	phosphopentose aldolase; fructose 1,6-diphosphate aldolase;			
KW	deoxyribokinase; nucleoside 2-deoxyribosyltransferase.			
OS	Salmonella typhi.			
XX	WO200114566-A2.			
XX	01-MAR-2001.			
XX	18-AUG-2000; 2000WO-EP08088.			
XX	20-AUG-1999; 99EP-0116425.			
XX	(HOFF ) ROCHE DIAGNOSTICS GMBH.			
PA	(INSP ) INST PASTEREUR.			
PA	(PHAR -) PHARMA-WALDHOF GMBH & CO KG.			
PI	Tischer W, Ihlenfeldt H, Barzu O, Sakamoto H, Pistotnik E;			
PI	Malliere P, Pochet S;			
DR	WPI; 2001-235026/24.			
DR	N-PSDB; AAF53444.			
XX	In vitro enzymatic synthesis of deoxyribonucleosides comprises reacting			
XX	deoxyribose 1-phosphate and a nucleobase to form a deoxyribonucleoside			
PT	and an inorganic phosphate			
PT	-			
XX	Disclosure: Page 59-61; 73pp; English.			
XX	The present sequence represents a deoxyribokinase enzyme. This enzyme			
CC	is involved in the biosynthesis of deoxyribonucleosides, and is			
CC	used in the method of the invention. The specification describes a			
CC	method for the in vitro enzymatic synthesis of deoxyribonucleosides.			
CC	The method comprises reacting deoxyribose 1-phosphate and a nucleobase			
CC	to form a deoxyribonucleoside and an inorganic phosphate. Enzymes which			
CC	may be used in the method of the invention include thymidine			
CC	phosphorylase, purine nucleoside phosphorylase, phosphopentose mutase,			
CC	phosphopentose aldolase, fructose 1,6-diphosphate aldolase,			
CC	deoxyribokinase, and nucleoside 2-deoxyribosyltransferase.			
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XX	Query Match 54.3%; Score 44; DB 22; Length 306;			
XX	Best Local Similarity 47.1%; Pred. NO. 18;			
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XX	Protein identification; signal transduction pathway; metabolic pathway;			
KW	hybridisation assay; genetic mapping; gene expression control; promoter;			

KW	germination sequence.
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 XX Protein identification: signal transduction pathway; metabolic pathway;  
 KM hybridisation assay; genetic mapping; gene expression control; promoter;  
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DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 54518.

KW Protein identification: signal transduction pathway; metabolic pathway;  
hybridisation assay: genetic mapping; gene expression control; promoter;  
termination sequence.

OS Arabidopsis thaliana.

PM EPI033405-A2.

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KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hydropathicity assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
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PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160860.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 25-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 26-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 51.9%; Score 42; DB 21; Length 332;  
Best Local Similarity 50.0%; Pred. No. 44;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 EEKPTLTAAXAPVYXNA 19  
| | | | |  
DB 291 EEKTPVEKKTGVPYKKA 308

## RESULT 11

ABB66926  
ID ABB66926 standard; Protein; 1012 AA.

AC ABB66926;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 27570.

XX Drosophila: developmental biology; cell signalling; insecticide;

KW pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.

DR N-PSDB; ABL11029.

XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
XX interactions -

PS Disclosure; SEQ ID NO 27570; 21bp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL3511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (AB57737-AB872072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1012 AA;

Query Match 50.6%; Score 41; DB 22; Length 1012;  
Best Local Similarity 53.3%; Pred. No. 2; 3e+02;  
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0.

QY 2 EEKPTLTAAXAPV 16  
| | | | |  
DB 695 EEVTPYNTAPHSPIV 709

## RESULT 12

ABB48482  
ID ABB48482 standard; Protein; 258 AA.

AC ABB48482;

DT 05-FEB-2002 (first entry)

DE Listeria monocytogenes protein #1186.

XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;

KW vitamin B12; bacterial infection; disease.

OS Listeria monocytogenes.

XX WO200177335-A2.

XX 18-OCT-2001.

PF 11-APR-2001; 2001WO-FR01118.

PR 11-APR-2000; 2000FR-0004629.

XX (INSP ) INST PASTEUR.

XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;

PI Dussurget O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P;

PI Daniels J, Goebel W, Kieft J, Kuhn M, Ng E, Vazquez-Boland JA;

PI Domínguez-Bernal G, Garrido-García P, Rierrez-Martínez A, Amend A;

PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;

PI Perez-Diaz J, Baquero F, García Del Portillo F, Gomez-Lopez N;

PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;

PI Rose M, Voss H;

WPI; 2002-010914/01.

XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment  
PT and prevention of Listeria and related bacterial infections, and  
PT related polypeptides -

XX Claim 6; SEQ ID NO 1187; 192bp; French.

XX The present invention relates to the genome sequence of Listeria  
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of  
CC it are useful for selecting probes and primers for detecting genes in L.  
CC monocytogenes and related organisms, and for studying genetic  
CC polymorphisms and other genomes. The present sequence is a protein  
CC encoded from the genome sequence of the present invention. Proteins  
CC expressed from the genome sequence are useful for raising specific  
CC antibodies, identification of L. monocytogenes and related organisms, and  
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin  
CC B12. The genome sequence and proteins encoded by it are also useful for  
CC selecting compounds that regulate gene expression and cell replication



CC 108, POL 128, GAG 148, VIF 158 and ENV 228.

Sequence 498 AA;

Query Match	Score	DB	Length
49.48;	40;	15;	498;

Best Local Similarity	44.48;	Pred. no. 1.3e+02;
Matches	8; Conservative	3; Mismatches 7; Indels 0; Gaps 0;

Matches 8; Conservative

2 EЕКТРЛТАХАРVXNA 19 QY

Db 119 EETSPRQTSQNPVTNA 136

RESULT 15

AAW93076 standard; Protein; 498 AA.  
ID

AC AAW93076;

19-MAY-1999 (first entry)

HIV isolate 5180 gag protein.

XX HIV-type retrovirus; MVP-5180/91; ECACC V 92092318; antigen; assay kit;  
KW

KW detection; antibody; immune deficiency; vaccine.

OS Human immunodeficiency virus

PN EP890642-A2.

PD 13-JAN-1999

PF 05-OCT-1993; 93EP-0116058.

PR 01-JUN-1993; 93DE-4318186

PR 22-OCT-1992; 92DE-4235718.

XX

11

(DADE-) DADE BEHRING MARBURG GMBH

PI Brunn AV, Eberle J, Guertler LG, Hauser H, Knapp S,

DR WPI; 1999-072878/07

AA  
PT New HIV-type retrovirus and corresponding cDNA, recombinant DNA and

deficiency and to prepare vaccines

Example 11; Fig 7; 39pp; German.

This invention describes the isolation of a novel HIV-type retrovirus

product can be used in an assay kit for detecting antibodies against

Western blot, ELISA or fluorescence immunoassay. MVP-5180/91, CDNA

deficiency and to prepare vaccines. This sequence represents an HIV

CC MVP 3100 gag protein.  
XX

sequence	450 aa
SD	100

Query Match	Pred. No.	1.5e+02;
Best Local Similarity	44.48;	

Matches	8;	Conse	valve				

QY 2 EERIPLEIAAAAPVANH 13  
||:|:|:|:|

Db 119 EETSPKQISQNYPLVINA 130

Search completed: March 14, 2003, 09:11:28

Job time : 38 secs

43

GenCore version 5.1.4.p5.4578  
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OK protein - protein search, using sw model

Run on: March 14, 2003, 09:10:49 ; Search time 14 seconds  
(without alignments)  
39.931 Million cell updates/sec

Title: US-09-359-426C-2  
Perfect score: 81  
Sequence: 1 XEERTPLTTAAKAPVXNA 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued\_Patents\_Aa.\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PTCUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/Backfilest.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	50.6	788	1 US-08-194-338-12	Sequence 12, Appl
2	40	49.4	498	1 US-08-470-202-59	Sequence 59, Appl
3	40	49.4	498	1 US-08-471-770-59	Sequence 59, Appl
4	40	49.4	498	2 US-08-468-059-59	Sequence 59, Appl
5	40	49.4	498	4 US-09-109-916-59	Sequence 59, Appl
6	37	45.7	456	2 US-08-624-125-20	Sequence 20, Appl
7	37	45.7	456	2 US-08-679-635A-4	Sequence 4, Appl
8	37	45.7	456	4 US-09-419-163-4	Sequence 4, Appl
9	36	44.4	19	3 US-08-943-173-8	Sequence 8, Appl
10	36	44.4	38	3 US-08-943-173-16	Sequence 16, Appl
11	36	44.4	71	3 US-08-943-173-2	Sequence 2, Appl
12	36	44.4	181	4 US-09-117-257-19	Sequence 19, Appl
13	36	44.4	181	4 US-08-945-476-19	Sequence 19, Appl
14	36	44.4	181	4 US-09-489-352-19	Sequence 19, Appl
15	36	44.4	182	4 US-09-117-257-48	Sequence 48, Appl
16	36	44.4	182	4 US-09-489-352-48	Sequence 48, Appl
17	36	44.4	236	4 US-09-134-001C-3558	Sequence 3558, Ap
18	36	44.4	355	2 US-08-458-555-2	Sequence 2, Appl
19	36	44.4	610	1 US-07-821-717B-6	Sequence 6, Appl
20	36	44.4	610	1 US-08-119-252B-6	Sequence 6, Appl
21	36	44.4	610	1 US-08-133-929A-11	Sequence 11, Appl
22	36	44.4	610	1 US-08-234-265A-11	Sequence 11, Appl
23	36	44.4	2318	4 US-09-091-219-24	Sequence 24, Appl
24	35	43.2	136	4 US-08-936-165A-461	Sequence 461, App
25	35	43.2	223	4 US-09-009-816-4	Sequence 4, Appl
26	35	43.2	223	4 US-09-071-035-204	Sequence 204, App
27	35	43.2	267	4 US-08-818-112-142	Sequence 142, App

28	35	43.2	267	4 US-08-818-111-137	Sequence 137, App
29	35	43.2	267	4 US-09-056-556-142	Sequence 142, App
30	35	43.2	267	4 US-09-072-596-137	Sequence 137, App
31	35	43.2	285	4 US-09-071-035-202	Sequence 202, App
32	35	43.2	344	6 5210183-2	Patent No. 5210183
33	35	43.2	367	4 US-09-009-816-2	Sequence 2, Appl
34	35	43.2	548	2 US-09-032-315-4	Sequence 4, Appl
35	35	43.2	548	2 US-08-993-318A-4	Sequence 4, Appl
36	35	43.2	548	4 US-09-399-886-4	Sequence 4, Appl
37	35	43.2	548	4 US-09-396-260-4	Sequence 4, Appl
38	35	43.2	558	4 US-09-576-281-4	Sequence 4, Appl
39	35	43.2	558	4 US-09-134-001C-4178	Sequence 4, Appl
40	35	43.2	662	1 US-07-841-651-4	Sequence 4, Appl
41	35	43.2	683	6 5210183-3	Patent No. 5210183
42	35	43.2	822	4 US-09-564-805-222	Sequence 222, App
43	35	43.2	826	4 US-09-564-805-2	Sequence 2, Appl
44	35	43.2	826	4 US-09-564-805-224	Sequence 224, App
45	35	43.2	826	4 US-09-564-805-226	Sequence 226, App

## ALIGNMENTS

```

RESULT 1
US-08-194-338-12
; Sequence 12, Application US/08194338
; Patent No. 5474898
;
GENERAL INFORMATION:
;
APPLICANT: Ventier, John C.
;
APPLICANT: Fraser, Claire M.
;
APPLICANT: McCombie, William R.
;
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
;
NUMBER OF SEQUENCES: 16
;
CORRESPONDENCE ADDRESS:
;
ADDRESSEE: Knobbie, Martens, Olson and Bear
;
STREET: 620 Newport Center Drive, Sixteenth Floor
;
CITY: Newport Beach
;
STATE: CA
;
COUNTRY: USA
;
ZIP: 92660
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Floppy disk
;
COMPUTER: IBM PC compatible
;
OPERATING SYSTEM: PC-DOS/MS-DOS
;
SOFTWARE: Patentin Release #1.0, Version #1.25
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/08/194,338
;
FILING DATE: 08-FEB-1994
;
CLASSIFICATION: 435
;
PRIOR APPLICATION DATA:
;
APPLICATION NUMBER: US 07/676,174
;
FILING DATE: 28-MAR-1991
;
ATTORNEY/AGENT INFORMATION:
;
NAME: Israelson, Ned A.
;
REGISTRATION NUMBER: 29,655
;
REFERENCE/DOCKET NUMBER: NIH101.001DV1
;
TELECOMMUNICATION INFORMATION:
;
TELEPHONE: (619) 235-8550
;
TELEFAX: (619) 235-0176
;
INFORMATION FOR SEQ ID NO: 12:
;
SEQUENCE CHARACTERISTICS:
;
LENGTH: 788 amino acids
;
TYPE: amino acid
;
STRANDEDNESS: single
;
TOPOLOGY: linear
;
MOLECULE TYPE: Protein
;
HYPOTHETICAL: NO
;
ANTI-SENSE: NO
;
FRAGMENT TYPE: Internal
;
US-08-194-338-12
;
Query Match 50.6%; Score 41; DB 1; Length 788;
Best Local Similarity 52.9%; Pred. No. 50;

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Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 3 EKTPLTTAAAPVYXNA 19

Db 602 EDOPTTTAAAPLASAA 618

## RESULT 2

US-08-470-202-59

Sequence 59, Application US/08470202

Patent No. 5759808

GENERAL INFORMATION:

APPLICANT: Guertler, Lutz G.

APPLICANT: Eberle, Josef

APPLICANT: Brunn, Albrecht V.

APPLICANT: Knapp, Stefan

TITLE OF INVENTION: Retrovirus from the HIV Group and Its

TITLE OF INVENTION: Use

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,202

FILING DATE: US

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/132,653

FILING DATE: 05-OCT-1993

APPLICATION NUMBER: DE P 42 33 646.5

FILING DATE: 06-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 35 718.7

FILING DATE: 22-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 44 541.8

FILING DATE: 30-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 43 18 186.4

FILING DATE: 01-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Michael J. Blake

REGISTRATION NUMBER: 37,096

REFERENCE/DOCKET NUMBER: 05495-0001-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 498 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-470-202-59

Query Match 49.4%; Score 40; DB 1; Length 498;

Best Local Similarity 44.4%; Pred. No. 44;

Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EKTPLTTAAAPVYXNA 19

Db 119 EETSPROTSONPIVTNA 136

Db 119 EETSPROTSONPIVTNA 136

## RESULT 3

US-08-471-770-59

Sequence 59, Application US/08471770

Patent No. 5770427

GENERAL INFORMATION:

APPLICANT: Guertler, Lutz G.

APPLICANT: Eberle, Josef

APPLICANT: Brunn, Albrecht V.

APPLICANT: Knapp, Stefan

APPLICANT: Hauser, Hans-Peter

TITLE OF INVENTION: Retrovirus from the HIV Group and Its

TITLE OF INVENTION: Use

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,770

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/132,653

FILING DATE: 05-OCT-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 33 646.5

FILING DATE: 06-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 35 718.7

FILING DATE: 22-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 44 541.8

FILING DATE: 30-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 43 18 186.4

FILING DATE: 01-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Carol P. Einaudi

REGISTRATION NUMBER: 32,220

REFERENCE/DOCKET NUMBER: 05495-0001-03000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 498 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-471-770-59

Query Match 49.4%; Score 40; DB 1; Length 498;

Best Local Similarity 44.4%; Pred. No. 44;

Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EKTPLTTAAAPVYXNA 19

Db 119 EETSPROTSONPIVTNA 136



RESULT 4

US-08-468-059-59

Sequence 59, Application US/08468059

Patent No. 5840480

GENERAL INFORMATION:

APPLICANT: Guerlier, Lutz G.

APPLICANT: Eberle, Josef

APPLICANT: Brunn, Albrecht V.

APPLICANT: Knapp, Stefan

APPLICANT: Hauser, Hans-Peter

TITLE OF INVENTION: Retrovirus from the HIV Group and Its

TITLE OF INVENTION: Use

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flunegan, Henderson, Farabow, Garrett &

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,059

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 33 646.5

FILING DATE: 06-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 35 718.7

FILING DATE: 22-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 44 541.8

FILING DATE: 30-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 43 18 186.4

FILING DATE: 01-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Carol P. Elnaui

REGISTRATION NUMBER: 32,220

REFERENCE/DOCKET NUMBER: 05495-0001-02000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 498 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-109-916-59

Sequence 59, Application US/09109916

Patent No. 6277561

GENERAL INFORMATION:

APPLICANT: Guerlier, Lutz G.

APPLICANT: Eberle, Josef

APPLICANT: Brunn, Albrecht V.

APPLICANT: Knapp, Stefan

APPLICANT: Hauser, Hans-Peter

TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE

TITLE OF INVENTION: Use

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flunegan, Henderson, Farabow, Garrett &

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/109,916

FILING DATE: 1998-07-02

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 33 646.5

FILING DATE: 1992-10-06

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 35 718.7

FILING DATE: 1992-10-22

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 44 541.8

FILING DATE: 1992-12-30

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 43 18 186.4

FILING DATE: 1993-06-01

ATTORNEY/AGENT INFORMATION:

NAME: Carol P. Elnaui

REGISTRATION NUMBER: 32,220

REFERENCE/DOCKET NUMBER: 05495-0001-02000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 498 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-109-916-59

Sequence 59, Application US/09109916

Patent No. 6277561

GENERAL INFORMATION:

APPLICANT: Guerlier, Lutz G.

APPLICANT: Eberle, Josef

APPLICANT: Brunn, Albrecht V.

APPLICANT: Knapp, Stefan

APPLICANT: Hauser, Hans-Peter

TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE

TITLE OF INVENTION: Use

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flunegan, Henderson, Farabow, Garrett &

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/109,916

FILING DATE: 1998-07-02

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 33 646.5

FILING DATE: 1992-10-06

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 35 718.7

FILING DATE: 1992-10-22

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 42 44 541.8

FILING DATE: 1992-12-30

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 43 18 186.4

FILING DATE: 1993-06-01

ATTORNEY/AGENT INFORMATION:

NAME: Carol P. Elnaui

REGISTRATION NUMBER: 32,220

REFERENCE/DOCKET NUMBER: 05495-0001-02000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 498 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE CHARACTERISTICS:  
LENGTH: 456 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-624-125-20

Query Match 45.7%; Score 37; DB 1; Length 456;  
Best Local Similarity 72.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 336 TTAAPVYXNA 346

RESULT 7  
US-08-679-635A-4  
Sequence 4, Application US/08679635A  
Patent No. 5985643

GENERAL INFORMATION:  
APPLICANT: Tomasz, Alexander  
APPLICANT: Delencastre, Hermenia  
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF  
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
FLOOR  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/679,635A  
FILING DATE: 10-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-141  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-343-1684  
TELEFAX: 201-487-5800  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-679-635A-4

Query Match 45.7%; Score 37; DB 2; Length 463;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 8 TTAAXAPVYXNA 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 382 TTAAPVYXNA 393

RESULT 8  
US-09-419-163-4  
Sequence 4, Application US/09419163

Patent No. 6391614  
GENERAL INFORMATION:  
APPLICANT: Tomasz, Alexander  
APPLICANT: Delencastre, Hermenia  
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF  
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
FLOOR  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/419,163  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/679,635  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-141  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-343-1684  
TELEFAX: 201-487-5800  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-09-419-163-4

Query Match 45.7%; Score 37; DB 4; Length 463;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 8 TTAAXAPVYXNA 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 382 TTAAPVYXNA 393

RESULT 9  
US-08-943-173-8  
Sequence 8, Application US/08943173  
Patent No. 6048538  
GENERAL INFORMATION:  
APPLICANT: Wang, Chang Yi  
APPLICANT: Shen, Fan  
TITLE OF INVENTION: PEPTIDES DERIVED  
TITLE OF INVENTION: FROM THE NON-STRUCTURAL PROTEINS OF  
TITLE OF INVENTION: FOOT AND MOUTH DISEASE VIRUS AS  
TITLE OF INVENTION: DIAGNOSTIC REAGENTS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,173

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lin, Maria C. H.

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4152

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

MOLECULE TYPE: linear

US-08-943-173-8

Query Match

Best Local Similarity 44.4%; Score 36; DB 3; Length 19;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 2 EKTPLTTAAKAPV 16

5 ERKPLKVKAKAPV 19

RESULT 10

US-08-943-173-16

Sequence 16, Application US/08943173

Patent No. 6048538

GENERAL INFORMATION:

APPLICANT: Wang, Chang YI

APPLICANT: Shen, Fan

APPLICANT: Chen, Pei De

TITLE OF INVENTION: PEPTIDES DERIVED

TITLE OF INVENTION: FROM THE NON-STRUCTURAL PROTEINS OF

TITLE OF INVENTION: FOOT AND MOUTH DISEASE VIRUS AS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Maria C. H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,173

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lin, Maria C. H.

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4152

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-943-173-16

Query Match

Best Local Similarity 44.4%; Score 36; DB 3; Length 58;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 2 EKTPLTTAAKAPV 16

31 ERKPLKVKAKAPV 45

RESULT 11

US-08-943-173-2

Sequence 2, Application US/08943173

Patent No. 6048538

GENERAL INFORMATION:

APPLICANT: Wang, Chang YI

APPLICANT: Shen, Fan

APPLICANT: Chen, Pei De

TITLE OF INVENTION: PEPTIDES DERIVED

TITLE OF INVENTION: FROM THE NON-STRUCTURAL PROTEINS OF

TITLE OF INVENTION: FOOT AND MOUTH DISEASE VIRUS AS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Maria C. H. Lin

STREET: 345 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/943,173

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lin, Maria C. H.

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4152

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 71 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-943-173-2

Query Match

Best Local Similarity 44.4%; Score 36; DB 3; Length 71;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 2 EKTPLTTAAKAPV 16

31 ERKPLKVKAKAPV 45

RESULT 12

US-09-117-257-19

Sequence 19, Application US/09117257

Patent No. 6214355

GENERAL INFORMATION:

APPLICANT: Hook, Magnus

APPLICANT: Guo, Betty

Page 6

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RESULT 14
US-09-489-352-19
; Sequence 19, Application US/09489352
; Patent No. 6312907
; GENERAL INFORMATION:

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Search completed: March 14, 2003, 09:13:13  
Job time : 15 secs

GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:12:34 ; Search time 13 Seconds  
(without alignments)  
67.365 Million cell updates/sec

Title: US-09-359-426c-2  
Perfect score: 81  
Sequence: 1 XEEKYPLTTAAAPVYXNA 19

Scoring table:  
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Gapop 10.0 , Capext 0.5

Searched: 199416 seqs, 46092074 residues  
Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB\_PEP.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB\_PEP.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB\_PEP.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	50.6	132	12	US-10-078-929-22
2	41	50.6	132	12	US-10-078-929-198
3	40	49.4	445	10	US-09-815-242-11701
4	40	49.4	498	9	US-09-886-156-59
5	40	49.4	498	9	US-09-886-150-59
6	40	49.4	498	9	US-09-886-149-59
7	40	49.4	498	9	US-09-886-159-59
8	39	48.1	155	10	US-09-952-432A-2
9	39	48.1	155	10	US-09-952-432A-16
10	39	48.1	233	9	US-09-738-626-5663
11	39	48.1	395	10	US-09-952-432A-19
12	39	48.1	395	10	US-09-952-432A-21
13	38	46.9	229	10	US-09-866-562-92
14	38	46.9	261	9	US-09-738-626-5209
15	38	46.9	277	10	US-09-764-846-214
16	37	45.7	456	10	US-09-323-998D-20
17	37	45.7	498	10	US-09-323-998D-57
18	37	45.7	500	10	US-09-323-998D-58
19	37	45.7	500	10	US-09-323-998D-59

20	36	44.4	501	10	US-09-323-998D-55	Sequence 55, Appl
21	35.5	43.8	175	10	US-09-925-301-964	Sequence 964, App
22	35	43.2	29	10	US-09-864-761-42235	Sequence 42235, A
23	35	43.2	136	10	US-09-939-980-461	Sequence 461, App
24	35	43.2	182	10	US-09-864-761-46598	Sequence 46598, A
25	35	43.2	156	9	US-09-738-626-6738	Sequence 6738, Ap
26	35	43.2	532	9	US-10-037-667-2	Sequence 2, Appl
27	35	43.2	548	9	US-09-869-877-4	Sequence 4, Appl
28	35	43.2	577	9	US-09-738-626-3648	Sequence 3648, Ap
29	35	43.2	822	9	US-09-988-626-222	Sequence 222, App
30	35	43.2	822	9	US-09-988-626-222	Sequence 222, App
31	35	43.2	826	9	US-09-988-626-224	Sequence 224, App
32	35	43.2	826	9	US-09-988-626-224	Sequence 224, App
33	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
34	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
35	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
36	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
37	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
38	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
39	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
40	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
41	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
42	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
43	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
44	35	43.2	826	9	US-09-988-626-226	Sequence 226, App
45	35	43.2	826	9	US-09-988-626-226	Sequence 226, App

ALIGNMENTS

RESULT 1  
US-10-078-929-22  
Sequence 22, Application US/10078929  
Patent No. US20020152497A1  
GENERAL INFORMATION:  
APPLICANT: Rafalski, Antoni  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Falco, Saverio Carl  
APPLICANT: Sakai, Hajime  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Odell, Joan T.  
APPLICANT: Meyers, Blake  
APPLICANT: Thorpe, Catherine  
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
TITLE OF INVENTION: Stress Response  
FILE REFERENCE: BB1357 US NA  
CURRENT APPLICATION NUMBER: US/10/078, 929  
PRIOR FILING DATE: 2002-02-19  
PRIOR APPLICATION NUMBER: 09/566,394  
PRIOR FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: 60/133038  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/133042  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/133427  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133437  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133428  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133438  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133436  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/137667  
PRIOR FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 22  
LENGTH: 132  
TYPE: PRT

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US-10-078-929-22
ORGANISM: Oryza sativa
Query Match          50.6%; Score 41; DB 12; Length 132;
Best Local Similarity 50.0%; Pred. No. 3.6;
Matches          9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY      2  EEKTPLTAAAXAPVYXNA 19
      |  |  |  |  |  |  |  |
Db      97  EAAPPTTTAAEAPAIAAA 114

RESULT 2
US-10-078-929-198
; Sequence 198, Application US/10078929
; Patent No. US20020152497A1
GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; TITLE OF INVENTION: Stress Response
; FILE REFERENCE: B81357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 198
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-078-929-198

Query Match          50.6%; Score 41; DB 12; Length 132;
Best Local Similarity 50.0%; Pred. No. 3.6;
Matches          9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY      2  EEKTPLTAAAXAPVYXNA 19
      |  |  |  |  |  |  |  |
Db      97  EAAPPTTTAAEAPAIAAA 114

RESULT 3
US-09-815-242-11701
; Sequence 11701, Application US/09815242
; Patent No. US20020061569A1
GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.

```

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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 11701
LENGTH: 445
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-815-242-11701

Query Match          49.4%;   Score 40;   DB 10;   Length 445;
Best Local Similarity 57.1%;   Pred. No. 22;
Matches      8;   Conservative      2;   Mismatches      4;   Indels      0;   Gaps      0.

QY      2  EKKPLTTAAAPV 15
      1:||||| 1 1
DB      382  EKKPLTTADMAI 395

RESULT 4
US-09-886-156-59
Sequence 59, Application US/09886156
Patent No. US20020155428A1
GENERAL INFORMATION:
APPLICANT: Gertler, Iulz G.
APPLICANT: Ederle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001-04
CURRENT APPLICATION NUMBER: US/09/886,156
CURRENT FILING DATE: 2001-06-22
CURRENT APPLICATION NUMBER: US/09/109,916
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: DE P 42 33 646.5
PRIOR FILING DATE: 1992-10-06
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR FILING DATE: 1992-10-22
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR FILING DATE: 1992-12-30
PRIOR APPLICATION NUMBER: DE P 43 18 186.4
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 59
LENGTH: 498
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-09-886-156-59

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Query Match 49.4%: Score 40; DB 9; Length 498;  
Best Local Similarity 44.4%: Pred. No. 25;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EEXTPLTTAAXAPVYXNA 19  
DB 119 EETSPROTSONYPIVTNA 136

RESULT 5  
US-09-886-150-59

; Sequence 59, Application US/09886150  
; Patent No. US20020172939A1  
; GENERAL INFORMATION:  
; APPLICANT: Guertler, Lutz G.  
; APPLICANT: Eberle, Josef  
; APPLICANT: Brunn, Albrecht V.  
; APPLICANT: Knapp, Stefan  
; APPLICANT: Hauser, Hans-Peter  
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE  
; FILE REFERENCE: 05495.0001-04  
; CURRENT APPLICATION NUMBER: US/09/886,150  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 09/109,916  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5  
; PRIOR FILING DATE: 1992-10-06  
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7  
; PRIOR FILING DATE: 1992-10-22  
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8  
; PRIOR FILING DATE: 1992-12-30  
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4  
; PRIOR FILING DATE: 1993-06-01  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: Patentl Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency virus  
US-09-886-150-59

Query Match 49.4%: Score 40; DB 9; Length 498;  
Best Local Similarity 44.4%: Pred. No. 25;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EEXTPLTTAAXAPVYXNA 19  
DB 119 EETSPROTSONYPIVTNA 136

RESULT 6  
US-09-886-149-59  
; Sequence 59, Application US/09886149  
; Publication No. US20030003442A1  
; GENERAL INFORMATION:  
; APPLICANT: Guertler, Lutz G.  
; APPLICANT: Eberle, Josef  
; APPLICANT: Brunn, Albrecht V.  
; APPLICANT: Knapp, Stefan  
; APPLICANT: Hauser, Hans-Peter  
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE  
; FILE REFERENCE: 05495.0001-04  
; CURRENT APPLICATION NUMBER: US/09/886,149  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 09/109,916  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5  
; PRIOR FILING DATE: 1992-10-06  
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7  
; PRIOR FILING DATE: 1992-10-22  
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8  
; PRIOR FILING DATE: 1992-12-30

; PRIOR APPLICATION NUMBER: DE P 43 18 186.4  
; PRIOR FILING DATE: 1993-06-01  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: Patentl Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency virus  
US-09-886-149-59

Query Match 49.4%: Score 40; DB 9; Length 498;  
Best Local Similarity 44.4%: Pred. No. 25;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EEXTPLTTAAXAPVYXNA 19  
DB 119 EETSPROTSONYPIVTNA 136

RESULT 7  
US-09-886-159-59  
; Sequence 59, Application US/09886159  
; Publication No. US20030003443A1  
; GENERAL INFORMATION:  
; APPLICANT: Guertler, Lutz G.  
; APPLICANT: Eberle, Josef  
; APPLICANT: Brunn, Albrecht V.  
; APPLICANT: Knapp, Stefan  
; APPLICANT: Hauser, Hans-Peter  
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE  
; FILE REFERENCE: 05495.0001-04  
; CURRENT APPLICATION NUMBER: US/09/886,159  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: 09/109,916  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5  
; PRIOR FILING DATE: 1992-10-06  
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7  
; PRIOR FILING DATE: 1992-10-22  
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8  
; PRIOR FILING DATE: 1992-12-30  
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4  
; PRIOR FILING DATE: 1993-06-01  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: Patentl Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: Human Immunodeficiency virus  
US-09-886-159-59

Query Match 49.4%: Score 40; DB 9; Length 498;  
Best Local Similarity 44.4%: Pred. No. 25;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EEXTPLTTAAXAPVYXNA 19  
DB 119 EETSPROTSONYPIVTNA 136

RESULT 8  
US-09-952-432A-2  
; Sequence 2, Application US/09952432A  
; Patent No. US20020150588A1  
; GENERAL INFORMATION:  
; APPLICANT: Allison, James P.  
; APPLICANT: Fasso, Marcelia  
; APPLICANT: Snastrl, Nilabh  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN  
; FILE REFERENCE: 018941-001110US  
; CURRENT APPLICATION NUMBER: US/09/952,432A  
; PRIOR FILING DATE: 2002-04-15

```

PRIORITY APPLICATION NUMBER: 60/234,472
PRIORITY FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 155
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SPAS-1 cDNA
US-09-952-432A-2

Query Match
Best Local Similarity: 48.1%; Score 39; DB 10; Length 155;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 TPLTTAAAPVY 16
: | | | | | | |
Db 60 SPTTTAATMPVY 71

SOUT 9
US-09-952-432A-16
Sequence 16, Application US/09952432A
Patent No. US2002015058A1
GENERAL INFORMATION:
APPLICANT: Allison, James P.
APPLICANT: Fasso, Marcelia
APPLICANT: Shastri, Nilabh
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
FILE REFERENCE: 018941-00110US
CURRENT FILING DATE: 2002-04-15
PRIORITY FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 155
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Predicted AA
OTHER INFORMATION: Sequence of mouse SPAS-1
US-09-952-432A-16

Query Match
Best Local Similarity: 48.1%; Score 39; DB 10; Length 155;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 TPLTTAAAPVY 16
: | | | | | | |
Db 60 SPTTTAATMPVY 71

RESULN 10
US-09-738-626-5663
Sequence 5663, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125

```

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CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO: 5663
LENGTH: 233
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5663

Query Match          48.1%; Score 39; DB 9; Length 233;
Best Local Similarity 66.7%; Pred. NO. 16;
Matches      8; Conservative      2; Mismatches      2; Indels      0; Gaps      0;

QY      5 TPLTTAAXAPV 16
      |||:| |||
DB      35 TPTTASAPAV 46

RESULT 11
US-09-952-432A-19
; Sequence 19, Application US/09952432A
; Patent No. US20020150588A1
; GENERAL INFORMATION:
; APPLICANT: Allison, James P.
; APPLICANT: Fasso, Marcelia
; APPLICANT: Shastri, Nilabh
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
; FILE REFERENCE: 018941-001100S
; CURRENT APPLICATION NUMBER: US/09/952,432A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/234,472
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tumor SPAS-1
US-09-952-432A-19

Query Match          48.1%; Score 39; DB 10; Length 395;
Best Local Similarity 66.7%; Pred. NO. 29;
Matches      8; Conservative      1; Mismatches      3; Indels      0; Gaps      0;

QY      5 TPLTTAAXAPV 16
      : |||| |||
DB      300 SPTTATMPV 311

RESULT 12
US-09-952-432A-21
; Sequence 21, Application US/09952432A
; Patent No. US20020150588A1
; GENERAL INFORMATION:
; APPLICANT: Allison, James P.
; APPLICANT: Fasso, Marcelia
; APPLICANT: Shastri, Nilabh
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
; FILE REFERENCE: 018941-001100S
; CURRENT APPLICATION NUMBER: US/09/952,432A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/234,472
;

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;; PRIOR FILING DATE: 2000-09-21  
;; NUMBER OF SEQ ID NOS: 32  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 21  
;; LENGTH: 395  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: No. US20020150588A1mal SPAS-1  
US-09-952-432A-21

Query Match 48.18; Score 39; DB 10; Length 395;  
Best Local Similarity 66.7%; Pred. No. 29;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 TPLTTAAAPV 16  
DB 300 SPTTAAATMPV 311

RESULT 13

US-09-866-562-92  
; Sequence 92, Application US/09866562  
; Patent No. US2002009758A1  
; GENERAL INFORMATION:  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Klee, Jennifer  
; APPLICANT: Switzer, Anne  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.502  
; CURRENT APPLICATION NUMBER: US/09/866.562  
; CURRENT FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 96  
; SEQ ID NO 92  
; LENGTH: 229  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-866-562-92

Query Match 46.9%; Score 38; DB 10; Length 229;  
Best Local Similarity 39.3%; Pred. No. 23;  
Matches 11; Conservative 1; Mismatches 4; Indels 12; Gaps 1;

OY 3 EKTPLTTAA-----XAPVYXN 18  
DB 109 EKTPLKTTATPLSLPKPRMDTAPVVAS 136

RESULT 14

US-09-738-626-5209  
; Sequence 5209, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIJO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738.626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162

;; PRIOR FILING DATE: 2000-04-07  
;; PRIOR APPLICATION NUMBER: JP 00/280988  
;; PRIOR FILING DATE: 2000-08-03  
;; NUMBER OF SEQ ID NOS: 7059  
;; SOFTWARE: PatentIn ver. 3.0  
;; SEQ ID NO 5209  
;; LENGTH: 261  
;; TYPE: PRT  
;; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-5209

Query Match 46.9%; Score 38; DB 9; Length 261;  
Best Local Similarity 70.0%; Pred. No. 27;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 PLTTAAAPV 15  
DB 149 PLTTAASAPV 158

RESULT 15

US-09-764-846-214  
; Sequence 214, Application US/09764846  
; Patent No. US20020102638A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT212  
; CURRENT APPLICATION NUMBER: US/09/764.846  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 348  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 214  
; LENGTH: 277  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (6)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (7)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (8)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (254)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (261)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (268)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (275)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (277)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-846-214

Query Match 46.9%; Score 38; DB 10; Length 277;  
Best Local Similarity 46.7%; Pred. No. 29;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 5 TPLTTAAAPVYXNA 19  
DB 120 JPVRAAPASPIVGA 134

Fri Mar 14 09:30:10 2003

us-09-359-426c-2.rapb

Search completed: March 14, 2003, 09:16:49  
Job time : 14 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:10:24 ; Search time 18 Seconds

(Without alignments)  
101.475 Million cell updates/sec

Title: US-09-359-426C-2

Perfect score: 81

Sequence: 1 XEKTPLTTAAKAPVYXNA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR73:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	77.8	482	2 B83113	catalase PA4236 (I
2	53	65.4	484	2 A58663	catalase (EC 1.11.
3	48	59.3	480	2 AB0148	catalase (EC 1.11.
4	46	56.8	262	2 T33408	hypothetical prote
5	45	56.8	128	2 E88400	protein H34124.2 (
6	45	55.6	128	2 JCI273	ribosomal protein
7	44	54.3	306	2 AE0963	probable carboxydr
8	44	54.3	427	2 F85436	hypothetical prote
9	43	53.1	483	2 S37055	catalase (EC 1.11.
10	42	51.9	105	2 A44639	catalase (EC 1.11.
11	42	51.9	321	2 T08462	hypothetical prote
12	42	51.9	436	2 T46107	hypothetical prote
13	41	50.6	132	2 T50779	hypothetical prote
14	41	50.6	482	2 S60757	copper chaperone h
15	40	49.4	171	2 T31478	catalase (EC 1.11.
16	40	49.4	252	2 H72469	hypothetical prote
17	40	49.4	258	2 AD1328	hypothetical prote
18	40	49.4	394	2 E87611	hypothetical prote
19	40	49.4	788	2 S05661	muscarinic acetylch
20	40	49.4	1360	2 T31674	hypothetical prote
21	39.5	48.8	405	2 JQ2147	OHP1 protein - mai
22	39	48.1	486	2 S10772	2-hydroxyisovaleryl
23	39	48.1	507	2 B87400	aldehyde dehydroge
24	39	48.1	527	2 S46088	hypothetical prote
25	38.5	47.5	1353	2 T26301	hypothetical prote
26	38	46.9	1658	2 D75489	growth-blocking pe
27	38	46.9	143	2 S68226	cytochrome c1, hem
28	38	46.9	307	2 T40089	phospholipase D (E
29	38	46.9	307	2 A51125	

30	38	46.9	348	2 S40750	hypothetical prote
31	38	46.9	474	2 E87650	peptidase, M20/M25
32	38	46.9	532	2 S40983	hypothetical prote
33	38	46.9	573	2 F81313	peptidase (M3 faml
34	38	46.9	684	2 T25603	hypothetical prote
35	38	46.9	695	2 D71283	probable translacl
36	38	46.9	747	2 F88561	protein F586A.11 (
37	38	46.9	1679	2 F88561	hypothetical prote
38	37.5	46.3	200	2 S48385	hypothetical prote
39	37	45.7	71	2 F72332	hypothetical prote
40	37	45.7	116	2 C83492	hypothetical prote
41	37	45.7	328	2 T03225	hypothetical prote
42	37	45.7	347	2 T35518	hypothetical prote
43	37	45.7	463	2 S72992	probable secretory
44	37	45.7	488	2 T42038	catalase (EC 1.11.
45	37	45.7	500	2 S72505	lycopene beta-cycl

## ALIGNMENTS

RESULT 1.

B83113

Catalase PA4236 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: B83113

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lathig, K.; I

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: AB2950; MUID:20437337; PMID:10964043

A:Accession: B83113

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-482 <STO>

A:Cross-references: GB:AE004841; GB:AE004091; NID:g9950451; PIDN:AA07624.1; GSPDB:GN

C:Genetics:

A:Gene: katA; PA4236

C:Superfamily: catalase

Query Match

Best Local Similarity 77.8%; Score 63; DB 2; Length 482;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKTPLTTAAKAPVYXN 18

DB 2 EKTPLTTAAKAPVYDN 18

RESULT 2

A58663

Catalase (EC 1.11.1.6) [validated] - Proteus mirabilis

C:Species: Proteus mirabilis

A:Variety: strain PR, peroxide resistant

C>Date: 19-Nov-1997 #sequence\_revision 21-Nov-1997 #text\_change 15-Sep-2000

R:Buyy, A.; Brachl, V.; Sterjades, R.; Chroboczek, J.; Thibault, P.; Gagnon, J.; Jc

J. Protein Chem. 14, 59-72, 1995

A>Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of

A:Reference number: A58663; MUID:95305957; PMID:7786407

A:Accession: A58663

A:Molecule type: protein

A:Residues: 1-484 <BUZ1>

A:Accession: B58663

A:Molecule type: DNA

A:Residues: 1-305, 'AE' <BUZ2>

R:Goulet, P.; Jouve, H.M.; Dideberg, O.

submitted to the Brookhaven Protein Data Bank, June 1996

A:Reference number: A67899; PDB:2CAE

A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 3-475

R:Gouet, P.; Jouve, H.M.; Hajdu, J.  
Submitted to the Brookhaven Protein Data Bank, June 1996  
A:Reference number: A67900; PDB:2CAF  
A:Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475  
A:Note: compound 1  
R:Gouet, P.; Jouve, H.M.; Hajdu, J.  
Submitted to the Brookhaven Protein Data Bank, June 1996  
A:Reference number: A67901; PDB:2CAG  
A:Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475  
A:Note: compound II, dithiothreitol reduced compound I  
R:Gouet, P.; Jouve, H.M.; Dideberg, O.  
Submitted to the Brookhaven Protein Data Bank, July 1996  
A:Reference number: A67902; PDB:2CAH  
A:Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475  
A:Note: native Fe(III) with NADPH  
R:Gouet, P.; Jouve, H.M.; Dideberg, O.  
J. Mol. Biol. 249, 933-954, 1995  
A:Title: Crystal structure of Proteus mirabilis PR catalase with and without bound NADPH  
A:Reference number: A58654; MUID:9531317; PMID:7791219  
A:Contents: annotation; X-ray crystallography, 2.2 angstroms  
Complex: homotetramer  
Function:  
A:Description: catalyzes the conversion of two of molecules of hydrogen peroxide to two  
A:Note: this enzyme has a tightly bound NADPH cofactor  
C:Superfamily: catalase  
C:Keywords: chromoprotein; heme; homotetramer; iron; metalloprotein; NADP; oxidoreductase  
F:53/Modified site: methionine sulfone (Met) #status experimental  
F:54\_93\_127/Active site: His, Ser, Asn #status predicted  
F:337/Binding site: heme iron (Tyr) (axial ligand) #status experimental

Query Match 65.4%; Score 53; DB 2; Length 484;  
Best Local Similarity 75.0%; Pred. No. 0.22;  
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 EKPPLTAAAPVYXN 18  
||| ||| ||| |||  
Db 2 EKKKLTAAAGAPVVDN 17

RESULT 3  
AB0148  
catalase (EC 1.11.1.6) [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AB0148  
R:Parfhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.  
deno-Parraga, A.M.; Chillingworth, T.; Cronin, A.; Davis, R.M.; Davis, P.; Dougan, G.;  
M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,  
Figure 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AB0148  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-480 <NUR>  
A:Cross-references: GB:AL590842; PIDN:CAC90045.1; PID:g159/9266; GSPDB:GN00175  
C:Genetics:  
A:Gene: katA  
C:Superfamily: catalase  
C:Keywords: oxidoreductase

Query Match 59.3%; Score 48; DB 2; Length 480;  
Best Local Similarity 68.8%; Pred. No. 1.6;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 EKPPLTAAAPVYXN 18  
||| ||| ||| |||  
Db 4 KKGGLTAAAGAPVVDN 19

RESULT 4  
T33408  
hypothetical protein H34124.2 - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T33408  
R:Latreille, P.; Wamsley, P.; O'Brien, D.  
Submitted to the EMBL Data Library, July 1998  
A:Description: The sequence of C. elegans cosmid H34124.  
A:Reference number: Z21340  
A:Accession: T33408  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-262 <LAT>  
A:Cross-references: EMBL:AF078784; PIDN:AAC26925.1; GSPDB:GN00021; CESP:H34124.2  
A:Experimental source: strain Bristol N2; clone H34124  
C:Genetics:  
A:Gene: CESP:H34124.2  
A:Map position: 3  
A:Note: Intron positions not resolved (incomplete sequence)

Query Match 56.8%; Score 46; DB 2; Length 262;  
Best Local Similarity 56.2%; Pred. No. 1.9;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 KPLPLTAAAPVYXNA 19  
||| ||| ||| |||  
Db 190 KPLPLTGGSSARVYINNA 205

RESULT 5  
E88400  
protein H34124.2 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: E88400  
R:Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio  
A:Reference number: A75000; MUID:99065613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C-  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;  
A:Accession: E88400  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-262 <STO>  
A:Cross-references: GB:chr\_III; PIDN:AAC26925.1; PID:g3329614; GSPDB:GN00021; CESP:H3  
C:Genetics:  
A:Gene: H34124.2  
A:Map position: 3

Query Match 56.8%; Score 46; DB 2; Length 262;  
Best Local Similarity 56.2%; Pred. No. 1.9;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 KPLPLTAAAPVYXNA 19  
||| ||| ||| |||  
Db 190 KPLPLTGGSSARVYINNA 205

RESULT 6  
JCI273  
ribosomal protein L7/L12 - Streptomyces antibioticus  
C:Species: Streptomyces antibioticus  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C:Accession: JCI273  
R:Parra, F.; Blanco, G.; Alonso, J.M.M.; Balbin, M.; Mendez, C.; Salas, J.A.  
Gene 118, 127-129, 1992  
A:Title: Cloning and sequence of a gene encoding the L7/L12 ribosomal protein equiva  
A:Reference number: JCI273; MUID:92380478; PMID:1511874  
A:Accession: JCI273  
A:Molecule type: DNA  
A:Residues: 1-128 <PAR>  
A:Cross-references: GB:M89911; NID:g153436; PIDN:AAA26811.1; PID:g153438  
C:Superfamily: Escherichia coli ribosomal protein L12  
C:Keywords: protein biosynthesis; ribosome

Query Match 55.6%: Score 45; DB 2; Length 128;  
Best Local Similarity 66.7%: Pred. No. 1.3;  
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 EKKPLTTAAKAPV 16  
||| : ||| |||  
Db 28 EKKPLTTAAKAPV 42

RESULT 7  
AE0963  
probable carbohydrate kinase STY3989 [imported] - Salmonella enterica subsp. enterica se  
C:Species: Salmonella enterica subsp. enterica serovar typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AE0963  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
A:Authors: Parkhill, J.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero  
A:Reference number: AB0502; PMID:11677608  
A:Accession: AE0963  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-306 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD03201.1; PID:g16504832; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY3989  
C:Superfamily: ribokinase

Query Match 54.3%: Score 44; DB 2; Length 306;  
Best Local Similarity 47.1%: Pred. No. 4.9;  
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 EKKPLTTAAKAPVXNA 19  
||| : ||| |||  
Db 84 EKKPLTTAAKAPVXNA 100

RESULT 8  
F85436  
hypothetical protein AT4g36970 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: F85436  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: AB5001; MUID:20083488; PMID:10617198  
A:Accession: F85436  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-427 <STO>  
A:Cross-references: GB:NC\_001268; NID:g7270646; PIDN:CAB80363.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: AT4g36970  
A:Map position: 4

Query Match 54.3%: Score 44; DB 2; Length 427;  
Best Local Similarity 60.0%: Pred. No. 7.1;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 EKKPLTTAAKAPV 16  
||| : ||| |||  
Db 208 EKKPLTTAAKAPV 222

RESULT 9  
S37055  
catalase (EC 1.11.1.6) alpha-2 chain - Streptomyces violaceus

C:Species: Streptomyces violaceus  
C:Date: 10-Dec-1993 #sequence\_revision 26-May-1995 #text\_change 04-Mar-2000  
C:Accession: S37055  
R:Facey, S.; van Pee, K.H.; Vining, L.C.  
submitted to the EMBL Data Library, August 1993  
A:Reference number: S37055  
A:Accession: S37055  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-483 <PAC>  
A:Cross-references: EMBL:X74791; NID:9397888; PIDN:CAA52796.1; PID:g581780  
A:Note: the source is designated as Streptomyces venezuelae  
C:Genetics:  
A:Start codon: GTG  
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase  
F:54/93.127/Active site: His, Ser, Asn #status predicted  
F:337/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match 53.1%: Score 43; DB 2; Length 483;  
Best Local Similarity 69.2%: Pred. No. 12;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 6 PLTTAAKAPVXN 18  
||| : ||| |||  
Db 5 PLTTAAKAPVXN 17

RESULT 10  
A4639  
catalase (EC 1.11.1.6) - Streptomyces coelicolor (fragments)  
C:Species: Streptomyces coelicolor  
C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 31-Oct-1997  
C:Accession: A4639  
R:Walker, G.  
submitted to the Protein Sequence Database, September 1994  
A:Reference number: A4639  
A:Accession: A4639  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-105 <WAL>  
C:Superfamily: catalase  
C:Keywords: oxidoreductase

Query Match 51.9%: Score 42; DB 2; Length 105;  
Best Local Similarity 69.2%: Pred. No. 3.4;  
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 6 PLTTAAKAPVXN 18  
||| : ||| |||  
Db 7 PLTTAAKAPVXN 19

RESULT 11  
T08462  
hypothetical protein F2206.250 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 22-Oct-1999  
C:Accession: T08462  
R:Queller, F.; Purnelle, B.; Boutry, M.; Goffeau, A.; Salanoubat, M.; Meves, H.W.; Ma  
submitted to the Protein Sequence Database, May 1999  
A:Reference number: Z16420  
A:Accession: T08462  
A:Molecule type: DNA  
A:Residues: 1-321 <QUE>  
A:Cross-references: EMBL:AL050300; GSPDB:GN00061; ATSP:F2206.250  
A:Experimental source: cultivar Columbia; BAC clone F2206  
C:Genetics:  
A:Gene: ATSP:F2206.250  
A:Map position: 3

Query Match 51.9%: Score 42; DB 2; Length 321;  
Best Local Similarity 50.0%: Pred. No. 12;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 2 EKPPLTTAAXAPVYXNA 19

Db 291 EKPTEKKTGVPVYKKA 308

## RESULT 12

T46107  
hypothetical protein T25B15.140 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000

C:Accession: T46107

R:Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K.

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23021

A:Accession: T46107

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-436 <ALC>

A:Cross-references: EMBL:AL132972

Experimental source: cultivar Columbia; BAC clone T25B15

C:Genetics:

A:Map position: 3

A:Introns: 418/1

A>Note: T25B15.140

Query Match

Best Local Similarity 51.9%; Score 42; DB 2; Length 436;  
Best Local Similarity 50.0%; Pred. No. 16;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 2 EKPPLTTAAXAPVYXNA 19

Db 395 EKPTEKKTGVPVYKKA 412

## RESULT 13

T50779  
copper chaperone homolog CCH [imported] - rice

C:Species: Oryza sativa (rice) #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000

C>Date: 21-Jul-2000

C:Accession: T50779

R:Himelblau, E.; Mira, H.; Jin, S.J.; Culotta, V.C.; Penarrubia, L.; Amasino, R.M.

Plant Physiol. 117, 1227-1234, 1998

A:Title: Identification of a functional homolog of the yeast copper homeostasis gene ATX

A:Reference number: Z24450; PMID:9701579

A:Accession: T50779

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-132 <HIM>

A:Cross-references: EMBL:AF198626; PIDN:AAF15285.1

Query Match

Best Local Similarity 50.6%; Score 41; DB 2; Length 132;  
Best Local Similarity 50.0%; Pred. No. 6.5;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 2 EKPPLTTAAXAPVYXNA 19

Db 97 EAAPPTTAAPAAIAAA 114

## RESULT 14

S60757  
catalase (EC 1.11.1.6) - Bordetella pertussis

C:Species: Bordetella pertussis

C>Date: 27-Apr-1996 #sequence\_revision 13-Mar-1997 #text\_change 04-Mar-2000

C:Accession: S60757

R:Deshaizer, D.; Wood, G.E.; Friedman, R.L.

Mol. Microbiol. 14, 123-130, 1994

A:Title: Molecular characterization of catalase from Bordetella pertussis: identification

A:Reference number: S60757; PMID:9511725; PMID:7830550

A:Accession: S60757

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-482 <DES>

A:Cross-references: EMBL:U07800; NID:9494943; PIDN:AA18481.1; PID:9494944

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994

C:Genetics:

A:Gene: cata

C:Superfamily: catalase

C:Keywords: Chromoprotein; heme; iron; metalloprotein; oxidoreductase

F;57,96,130/Active site: His, Ser, Asn #status predicted

F;340/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match

Best Local Similarity 50.6%; Score 41; DB 2; Length 482;  
Best Local Similarity 75.0%; Pred. No. 27;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 LTTAAXAPVYXN 18

Db 9 LTTAAGAPVADN 20

## RESULT 15

T31478  
hypothetical protein F56F12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999

C:Accession: T31478

R:Ainscough, R.

submitted to the EMBL Data Library, October 1999

A:Reference number: Z21039

A:Accession: T31478

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-171 <WIL>

A:Cross-references: EMBL:Z82273; PIDN:CAB54978.1; GSPDB:GN00022; CESP:F56F12.1

A:Experimental source: clone F56F12

C:Genetics:

A:Gene: CESP:F56F12.1

A:Map position: 4

A:Introns: 16/2; 50/1

Query Match

Best Local Similarity 49.4%; Score 40; DB 2; Length 171;  
Best Local Similarity 53.3%; Pred. No. 13;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 5 TPLTTAAXAPVYXNA 19

Db 73 TPTTTAAPAAIAA 87

Search completed: March 14, 2003, 09:12:52

Job time : 21 secs



```

DR InterPro: IPR002226; Catalase.
DR Pfam: PF00199; catalase_1.
DR PRINTS: PR00067; CATALASE.
DR PRODOM: PD000510; Catalase_1.
DR PROSITE: PS00437; CATALASE_1; 1.
DR PROSITE: PS00438; CATALASE_2; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
KW Complete proteome.
FT ACET SITE 55 55 BY SIMILARITY.
FT ACET SITE 128 128 BY SIMILARITY.
FT BINDING 338 338 PROXIMAL HEME LIGAND (BY SIMILARITY).
SO SEQUENCE 482 AA; 55589 MW; 845BAA647CAB414 CRC64;

Query Match
Best Local Similarity 77.8%; Score 63; DB 1; Length 482;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 EKKPLTTAAAPVYVN 18
DB 2 EKKRLTTAAGAPVVDN 18

RESULT 2
ID CATA_PROM1 STANDARD; PRT; 484 AA.
AC P42321;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Catalase (EC 1.11.1.6).
GN KATA.
OS proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE, AND SEQUENCE OF 1-305 FROM N.A.
RC STRAIN=PR;
RX MEDLINE=95305957; PubMed=7786407;
RA Buzy A., Bracchi V., Steriades R., Chroboczek J., Thibault P.,
RA Gagnon J., Jouve H.-M., Hudry-Clergeon G.;
RT "Complete amino acid sequence of Proteus mirabilis PR catalase.
RT occurrence of a methionine sulfone in the close proximity of the
RT active site."
RT J. Protein Chem. 14:59-72(1995).
RL [2]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RP STRAIN=PR;
RC MEDLINE=95311317; PubMed=7791219;
RC Gouet P., Jouve H.-M., Dideberg O.;
RT "Crystal structure of Proteus mirabilis PR catalase with and without
RT bound NADPH."
RL J. Mol. Biol. 249:933-954(1995).
CC -1- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES
CC TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
CC -1- COFACTOR: HEME GROUP AND NADP.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MASS SPECTROMETRY: MW=55643; MW_ERR=5; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
DR PDB: 2CAF; 08-DEC-96.
DR PDB: 2CAF; 07-DEC-96.
DR PDB: 2CAG; 07-DEC-96.
DR PDB: 2CAH; 11-JAN-97.
DR InterPro: IPR002226; Catalase.
DR Pfam: PF00199; catalase_1.
DR PRINTS: PR00067; CATALASE.
DR PRODOM: PD000510; Catalase_1.
DR PROSITE: PS00437; CATALASE_1; 1.
DR PROSITE: PS00438; CATALASE_2; 1.
KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP;
KW 3D-structure.

```

```

FT MOD_RES 53 53 METHIONINE SULFONE.
FT ACET SITE 54 54
FT ACET SITE 127 127
FT BINDING 337 337 PROXIMAL HEME LIGAND.
SO SEQUENCE 484 AA; 55614 MW; ADC25F3CD41E5CC50 CRC64;

Query Match
Best Local Similarity 65.4%; Score 53; DB 1; Length 484;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 EKKPLTTAAAPVYVN 18
DB 2 EKKRLTTAAGAPVVDN 17

RESULT 3
ID RL7_STRAT STANDARD; PRT; 128 AA.
AC P29342;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L7/L12.
GN RPL7.
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92380478; PubMed=1511874;
RA Parra F., Blanco G., Alonso J.M., Balbin M., Mendez C., Salas J.A.;
RT "Cloning and sequence of a gene encoding the L7/L12 ribosomal protein
RT equivalent of Streptomyces antibioticus."
RT Gene 118:127-129(1992).
CC -1- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS
CC INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR
CC ACCURATE TRANSLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: M89911; AAA26811.1; .
DR PIR: JCI273; JCI273.
DR HSSP: P02392; ICTF.
DR InterPro: IPR000206; Ribosomal_L12.
DR Pfam: PF00542; Ribosomal_L12; 1.
DR PRODOM: PD001326; Ribosomal_L12; 1.
DR TIGRFAMs: TIGR00855; L12; 1.
KW Ribosomal protein.
SO SEQUENCE 128 AA; 13272 MW; F5C3BE4F45D606E8 CRC64;

Query Match
Best Local Similarity 55.6%; Score 45; DB 1; Length 128;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 EKKPLTTAAAPV 16
DB 28 EKKPLTTAAAPV 42

RESULT 4
ID BCA_STRVL STANDARD; PRT; 483 AA.
AC P33569;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

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CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U07800; AAA18481.1; -.
CC HSSP; P42321; 2CAE.
CC InterPro; IPR002226; Catalase.
CC Pfam; PF00199; catalase; 1.
CC PRINTS; PR00067; CATALASE.
CC ProDom; PD000510; Catalase; 1.
CC PROSITE; PS00437; CATALASE_1; 1.
CC PROSITE; PS00438; CATALASE_2; 1.
CC Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
CC ACT_SITE 57
CC ACT_SITE 130 130 BY SIMILARITY.
CC BINDING 340 340 PROXIMAL HEME LIGAND (BY SIMILARITY).
CC SEQUENCE 482 AA; 54508 MW; 7CB73E08975C219F CRC64;
CC -----
CC Query Match 50.6%; Score 41; DB 1; Length 482;
CC Best Local Similarity 75.0%; Pred. No. 14;
CC Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CC -----
QY 7 LTTAAXAPVYXN 18
CC ||||| ||| |
DB 9 LTTAAGAPVADN 20
CC -----
RESULT 6
ACM1_DROME STANDARD: PRT; 722 AA.
AC ID ACM1_DROME
AC P16395;
DT 01-AUG-1990 (Rel. 15. Created)
DT 01-AUG-1990 (Rel. 15; Last sequence update)
DT 01-NOV-1997 (Rel. 35; Last annotation update)
DE Muscarinic acetylcholine receptor DML.
GN ACRC OR MACR-60C.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
OX [1]
RN RP SEQUENCE FROM N.A.
RN STRAIN-Oregon-R;
RX MEDLINE=90046926; PubMed=2510174;
RA Shapiro R.A., Wakimoto B.T., Subers E.M., Nathanson N.M.;
RT "Characterization and functional expression in mammalian cells of
RT genomic and cDNA clones encoding a Drosophila muscarinic
RT acetylcholine receptor.";
RL proc. Natl. Acad. Sci. U.S.A. 86:9039-9043(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90005981; PubMed=2507354;
RA Onal T., Fitzgerald M.G., Atakawa S., Gocayne J.D., Urquhart D.A.,
RA Hall L.M., Fraser C.M., McCombie W.R., Venter J.C.;
RT "Cloning, sequence analysis and chromosome localization of a
RT drosophila muscarinic acetylcholine receptor.";
RL FEBS Lett. 255:219-225(1989).
CC -1- FUNCTION: "THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHODIESTERASES AND MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
CC PI TURNOVER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----

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DR EMBL; M27495; AAA85449.1; -  
 DR EMBL; M23412; AAA28676.1; ALT\_INIT.  
 DR PIR; A36191; A36191.  
 DR PIR; S05661; S05661.  
 DR FlyBase; FBgn0000037; MACR-60C.  
 DR InterPro; IPR00276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCR\_Rhodopsn.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS50262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 DR Posttranslational; Multigene family; G-protein coupled receptor.  
 KW phosphorylation; Multigene family; G-protein coupled receptor.

FT DOMAIN 1 26  
 FT TRANSMEM 27 49  
 FT DOMAIN 50 60  
 FT TRANSMEM 61 81  
 FT DOMAIN 82 100  
 FT TRANSMEM 101 120  
 FT DOMAIN 121 140  
 FT TRANSMEM 141 162  
 FT DOMAIN 163 184  
 FT TRANSMEM 185 208  
 FT DOMAIN 209 234  
 FT TRANSMEM 235 256  
 FT DOMAIN 257 272  
 FT TRANSMEM 273 293  
 FT DOMAIN 294 312  
 FT TRANSMEM 313 333  
 FT DOMAIN 334 352  
 FT TRANSMEM 353 373  
 FT DOMAIN 374 392  
 FT TRANSMEM 393 413  
 FT DOMAIN 414 432  
 FT TRANSMEM 433 453  
 FT DOMAIN 454 472  
 FT TRANSMEM 473 493  
 FT DOMAIN 494 512  
 FT TRANSMEM 513 533  
 FT DOMAIN 534 552  
 FT TRANSMEM 553 573  
 FT DOMAIN 574 592  
 FT TRANSMEM 593 613  
 FT DOMAIN 614 632  
 FT TRANSMEM 633 653  
 FT DOMAIN 654 672  
 FT TRANSMEM 673 693  
 FT DOMAIN 694 712  
 FT TRANSMEM 713 733  
 FT DOMAIN 734 752  
 FT TRANSMEM 753 773  
 FT DOMAIN 774 792  
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RX MEDLINE=9831655; PubMed=9654083;
RA Hayakawa Y., Noguchi H.;
RT "Growth-blocking peptide expressed in the insect nervous system:
RT cloning and functional characterization.";
RL Eur. J. Biochem. 253:810-816(1998).
RN [3]
RP STRUCTURE BY NMR OF 121-143.
RC TISSUE=Hemolymph;
RX MEDLINE=99107831; PubMed=9890941;
RA Aizawa T., Fujitani N., Hayakawa Y., Ohnishi A., Ohkubo T., Kumaki Y.,
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RT "Solution structure of an insect growth factor, growth-blocking
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CC -1- FUNCTION: BIOGENIC PEPTIDE THAT PREVENTS, IN LEPIDOPTERAN, THE
CC ONSET OF METAMORPHOSIS FROM LARVA TO PUPA, THIS GROWTH-BLOCKING
CC PEPTIDE HAS REPRESSIVE ACTIVITY AGAINST JUVENILE HORMONE ESTERASE.
CC -1- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
CC -----
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DR EMBL: S80564; AAB35742.1; -;
DR EMBL: AB012284; BAA32793.1; -;
DR PDB: 1BQF; 09-DEC-98.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
KW Hemolymph; signal; 3D-structure.
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DT 01-FEB-1994 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Phospholipase D precursor (EC 3.1.4.4) (PUD) (Choline phosphatase).
GN PUD.
OS Corynebacterium pseudotuberculosis.
OC Bacteria: Actinobacteria: Actinobacteria (class): Actinobacteridae:
OC Actinomycetales: Corynebacterinae: Corynebacteriaceae:
OC Corynebacterium.
OX NCBI_TaxID=1719;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-47.
RX MEDLINE=90170833; PubMed=2407718;
RA Hodgson A.L.M., Bird P., Nisbet I.T.;
RT "Cloning, nucleotide sequence, and expression in Escherichia coli of
RT the phospholipase D gene from Corynebacterium pseudotuberculosis.";
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RP SEQUENCE FROM N.A.
OC STRAIN=BIOLOG 0.4;

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 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Biovar equi / Isolate 155;  
 RX MEDLINE-95255653; PubMed-7737503;  
 RA McNamara P.J., Cuevas W.A., Songer J.G.;  
 RT "Toxic phospholipases D of *Corynebacterium pseudotuberculosis*, C.  
 RL *ulcerans* and *Arcanobacterium haemolyticum*: cloning and sequence  
 homology."; Gene 156:113-118(1995).  
 RN [4]  
 RP MOTAGENESIS.  
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 CC -1- FUNCTION: VIRULENCE FACTOR AFFECTING BACTERIAL DISSEMINATION AND  
 CC SURVIVAL WITHIN THE HOST. HAS MAGNESIUM-DEPENDENT SPHINGOMELINASE  
 CC AND HEMOLYTIC ACTIVITY.  
 CC -1- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)O = choline + a  
 CC phospholipate.  
 CC -1- SIMILARITY: TO OTHER *CORYNEBACTERIUM* PHOSPHOLIPASES D.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: L16587; AAA64910.1; -;  
 DR EMBL: L16586; AAA99867.1; -;  
 DR PIR: A35125; A35125.  
 KW Hydrolyase; Lipid degradation; Magnesium; Virulence; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 307  
 FT ACT\_SITE 44 44  
 FT VARIANT 5 6  
 FT VARIANT 8 8  
 FT VARIANT 189 189  
 FT VARIANT 205 205  
 FT VARIANT 270 270  
 FT VARIANT 277 277  
 SO SEQUENCE 307 AA; 33864 MW; D3B1334E6FC9875 CRC64;  
 Query Match 46.9%; Score 38; DB 1; Length 307;  
 Best Local Similarity 61.5%; Pred. No. 28;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 6 LTTTAAAPVYN 18  
 DB 18 PTCNMAAPVYN 30  
 RESULT 14  
 CATA\_PSEPU STANDARD; PRT; 479 AA.  
 ID CATA\_PSEPU  
 AC 059714;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE Catalase (EC 1.11.1.6).  
 GN CATA OR CATA.  
 OS *Pseudomonas putida*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 CC Pseudomonas.  
 NCBI\_TaxID=303;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Corvallis;  
 RX MEDLINE-98019091; PubMed-9358059;  
 RA Kim Y.C., Miller G.D., Anderson A.J.;  
 RT "Identification of adjacent genes encoding the major catalase and a  
 RL bacterioferritin from the plant-beneficial bacterium *Pseudomonas*  
 Gene 199:219-224(1997).  
 CC -1- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN. SERVES  
 CC TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.  
 CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) - O(2) + 2 H(2)O.  
 CC -1- COFACTOR: HEME GROUP.  
 CC -1- ENZYME REGULATION: ACTIVATED BY PEROXIDE.  
 CC -1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.  
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 CC -----  
 DR EMBL: U63511; AAB86219.1; -;  
 DR HSSP; P4321; ZCAE.  
 DR InterPro; IPR002226; Catalase.  
 DR Pfam; PF00199; catalase: 1.  
 DR PRINTS; PR00067; CATALASE.  
 DR PRODOM; PD000510; Catalase.  
 DR PROSITE; PS00437; CATALASE\_1; 1.  
 DR PROSITE; PS00438; CATALASE\_2; 1.  
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.  
 FT ACT\_SITE 53 53  
 FT ACT\_SITE 126 126  
 FT BINDING 336 336  
 SO SEQUENCE 479 AA; 53381 MW; EF3CBDE67778571 CRC64;  
 Query Match 46.9%; Score 38; DB 1; Length 479;  
 Best Local Similarity 66.7%; Pred. No. 44;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 LTTTAAAPVYN 18  
 DB 5 LTTTAAAPVYN 16  
 RESULT 15  
 EFG1\_TREPA STANDARD; PRT; 695 AA.  
 ID EFG1\_TREPA  
 AC 083748;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Elongation factor G 1 (EF-G 1).  
 GN FUS4 OR FUS4-2 OR TP0767.  
 OS *Treponema pallidum*.  
 OC Bacteria; Spirochaetales; Spirochaetaceae; *Treponema*.  
 NCBI\_TaxID=160;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Nichols;  
 RX MEDLINE-96332770; PubMed-9665876;  
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,  
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,  
 RA Sodergren E., Hardham J.M., McLeod M.F., Salzberg S., Peterson J.,  
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Ullrich J.,  
 RA McDonald L., Arlisch P., Bowman C., Cotton M.D., Fujii C., Garland S.,  
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weldman J., Smith H.O.,  
 RA Venter J.C.;  
 RT "Complete genome sequence of *Treponema pallidum*, the syphilis  
 RL spirochete."; Science 281:375-388(1998).

```

CC CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
CC CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC CC RIBOSOME.
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC CC EF-G/EF-2 SUBFAMILY.
CC CC -----
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CC CC -----
CC CC EMBL: AE001248; AAC65735.1; -.
CC CC HSSP: P13551; 2EPFG.
CC CC TIGR: TP0767; -.
CC CC InterPro: IPR004540; EF-G.
CC CC InterPro: IPR000640; EFG_C.
CC CC InterPro: IPR004161; EFTU_D2.
CC CC InterPro: IPR00795; EF_GTPbind.
CC CC InterPro: IPR005225; Small_GTP.
CC CC Pfam: PF00009; GTP_EFTU.1.
CC CC Pfam: PF00679; EFG_C.1.
CC CC Pfam: PF03144; GTP_EFTU_D2.1.
CC CC PRINTS: PR00315; ELONGATNFACT.
CC CC TIGRPFAMS: TIGR00231; small GTP. 1.
CC CC TIGRPFAMS: TIGR00404; EF-G. 1.
CC CC PROSITE: PS00301; EFACOR_GTP. 1.
CC CC Elongation factor: Protein biosynthesis; GTP-binding;
CC CC Multigene family; Complete proteome.
CC CC NP_BIND 15 122 GTP (BY SIMILARITY).
CC CC FT NP_BIND 82 86 GTP (BY SIMILARITY).
CC CC FT NP_BIND 136 139 GTP (BY SIMILARITY).
CC CC SEQUENCE 695 AA; 76831 MW; 4652989BFE97E4E CRC64;

```

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## OM protein - protein search, using sw model

Run on: March 14, 2003, 09:09:54 ; Search time 29 Seconds  
(without alignments)  
134.996 Million cell updates/sec

Title: US-09-359-426c-2

Sequence: 1 XEEKPLTTTAXAPVXNA 19

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPREMBL\_21:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	48	59.3	480 16 08ZGS4	08ZGS4 Yersinia pe
2	46	56.8	458 5 076672	076672 caenorhabd
3	45	55.6	484 2 09RG14	09RG14 actinobacti
4	44	54.3	306 16 08XGWS	08XGWS salmonella
5	44	54.3	314 2 09A119	09A119 escherichia
6	44	54.3	427 10 09A400	09A400 arabidopsis
7	44	54.3	427 10 023188	023188 arabidopsis
8	43	53.1	506 2 P77924	P77924 pseudomonas
9	43	53.1	1240 12 09DMH8	09DMH8 rat cytochrome
10	42	51.9	210 2 09RND2	09RND2 streptococ
11	42	51.9	211 2 09X6X8	09X6X8 streptococ
12	42	51.9	436 10 09FT45	09FT45 arabidopsis
13	42	51.9	487 16 09RJK9	09RJK9 streptomyces
14	41	50.6	132 10 09SE04	09SE04 oryza sativ
15	41	50.6	417 2 054272	054272 streptomyces
16	41	50.6	663 17 08ZGX0	08ZGX0 pyrobaculum

17	41	50.6	1012 5 09V745	09V745 drosophila
18	40	49.4	171 5 09U3E3	09U3E3 caenorhabd
19	40	49.4	212 5 09U4T3	09U4T3 ceratilis c
20	40	49.4	252 17 09V984	09V984 aeopyrum p
21	40	49.4	258 16 08Y5M9	08Y5M9 listeria mo
22	40	49.4	394 16 09A4B0	09A4B0 caulobacter
23	40	49.4	477 16 09RD97	09RD97 streptomyces
24	40	49.4	498 15 079665	079665 human immun
25	40	49.4	554 5 09B1H5	09B1H5 halocynthia
26	40	49.4	788 5 09M1B0	09M1B0 drosophila
27	40	49.4	846 13 057577	057577 cynops pyr
28	40	49.4	1360 5 002006	002006 drosophila
29	40	49.4	1473 5 09VHP9	09VHP9 drosophila
30	39.5	48.8	405 10 003462	003462 zea mays (m
31	39.5	48.8	1793 5 09W596	09W596 drosophila
32	39	48.1	255 10 091GM5	091GM5 oryza sativ
33	39	48.1	395 11 091217	091217 mus musculu
34	39	48.1	395 11 08R3V5	08R3V5 mus musculu
35	39	48.1	410 2 09FD09	09FD09 streptococ
36	39	48.1	419 16 08ZNG4	08ZNG4 salmonella
37	39	48.1	484 12 09W4U2	09W4U2 human adeno
38	39	48.1	484 16 09CPK5	09CPK5 pasteurella
39	39	48.1	507 16 09ABX1	09ABX1 caulobacter
40	39	48.1	518 13 09PTV0	09PTV0 cyprinus ca
41	39	48.1	572 10 091JG2	091JG2 arabidopsis
42	39	48.1	952 12 099174	099174 human adeno
43	39	48.1	1353 5 018182	018182 caenorhabd
44	39	48.1	4900 5 09N541	09N541 caenorhabd
45	38.5	47.5	842 5 09VJH6	09VJH6 drosophila

## ALIGNMENTS

## RESULT 1

ID 08ZGS4

AC 08ZGS4

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Catalase (EC 1.11.1.6).

GN KATA OR YPO1207.

OS Yersinia pestis.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Yersinia.

OX NCBI\_TaxID=632.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CO-92 / BIOVAR ORIENTALIS;

RX MEDLINE=21470413; PubMed=11586360;

RA Parkhill J., Wren B.W., Thomson N.R., Tiliak R.W., Holden M.T.G.,

RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,

RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,

RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

RA Feltham T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V.,

RA Leather S., Mouton S., Oyston P.C.F., Quail M., Rutherford K.,

RA Simmons M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,

RT "Genome sequence of Yersinia pestis, the causative agent of plague."

RL Nature 413:523-527(2001).

DR EMBL: A014147; CAC90045.1; -

DR InterPro: IPR002226; Catalase.

DR Pfam: PF00109; Catalase.1.

DR PRODOM: PD000510; Catalase.1.

DR PROSITE: PS00438; CATALASE\_2.1.

KW Oxidoreductase; Peroxidase; Complete proteome.

SQ SEQUENCE 480 AA: 55023 MW: 27A72FBAF096347E CRC64;

QY Query Match 59.3%; Score 48; DB 16; Length 480;

Best Local Similarity 68.8%; Pred. No. 8.6;

Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

DB      4 KKGITRACAPVDN 19
RESULT 2
ID      076672      PRELIMINARY;      PRT;      458 AA.
AC      076672:
DT      01-NOV-1998 (TReMBLrel. 08, Created)
DT      01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT      01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE      Hypothetical 47.3 kDa protein.
GN      H34124.2.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RC      MEDLINE=99069613; PubMed=9851916;
None:
RT      "Genome sequence of the nematode C. elegans: a platform for
RT      investigating biology. The C. elegans Sequencing Consortium.";
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RA      Latreille P., Wamsley P., O'Brien D.;
RT      "The sequence of C. elegans cosmid H34124.";
RN      [3]
RP      Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RA      SEQUENCE FROM N.A.
RC      STRAIN-BRISTOL N2;
RC      Waterston R.;
RT      Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AF078784; AAK18967.1; -
KM      Hypothetical protein.
SQ      SEQUENCE 458 AA; 47285 MW; 2AF5BC94EDA0C324 CRC64;

Query Match      56.8%; Score 46; DB 5; Length 458;
Best Local Similarity 56.2%; Pred. No. 17;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY      4 KTLPTTAAAPVYXNA 19
DB      386 KTLPTSGSSARVINNA 401

```

```

CC      -!- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
CC      SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
CC      PEROXIDE (BY SIMILARITY).
CC      -!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
DR      EMBL: AF162654; AAF17882.1; -.
DR      HSSP: P42321; 2CAE.
DR      InterPro: IPR002226; Catalase.
DR      Pfam: PF00199; catalase; 1.
DR      PRINTS: PR00067; CATALASE.
DR      ProDom: PD000510; Catalase; 1.
DR      PROSITE: PS00437; CATALASE.1; 1.
DR      PROSITE: PS00438; CATALASE.2; 1.
KM      Heme: Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SQ      SEQUENCE 484 AA; 54961 MW; DDE523AR257D8CB CRC64;

Query Match      55.6%; Score 45; DB 2; Length 484;
Best Local Similarity 83.3%; Pred. No. 27;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      7 LTTAAXAPVYXN 18
DB      14 LTTAAGAPVDN 25
RESULT 4
O8XGWS      PRELIMINARY;      PRT;      306 AA.
AC      O8XGWS:
DT      01-MAR-2002 (TReMBLrel. 20, Created)
DT      01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT      01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE      Putative sugar kinase, ribokinase family (EC 2.7.1.15) (Putative
DE      carbohydrate kinase).
GN      STM3793 OR STM3989.
OS      Salmonella typhimurium, and
OS      Salmonella typhi.
OC      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC      Salmonella.
OX      NCBI_TaxID=602, 601;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      SPECIES-S. typhimurium, STRAIN-LT2 / SSGC1412 / ATCC 700720;
RC      MEDLINE=21534948; PubMed=11677609;
RA      McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA      Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA      Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA      Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA      Waterston R., Wilson R.K.;
RT      "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT      LT2.";
RL      Nature 413:852-856(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      SPECIES-S. typhi, STRAIN-CT18;
RC      MEDLINE=21534947; PubMed=11677608;
RA      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA      Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA      Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA      Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA      Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsis K.,
RA      Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA      Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA      Whitehead S., Barrrell B.G.;
RT      "Complete genome sequence of a multiple drug resistant Salmonella
RT      enterica serovar Typhi CT18.";
RL      Nature 413:848-852(2001).
DR      EMBL: AE008876; AAL22651.1; -.
DR      EMBL: AL627280; CAD03201.1; -.
DR      InterPro: IPR002173; PfKB.
DR      Pfam: PF00294; PfKB; 1.
KM      Kinase; Transferase; Hypothetical protein; Complete proteome.
SQ      SEQUENCE 306 AA; 33229 MW; 142A0289F2D1B953 CRC64;

```



Query Match 54.3% Score 44: DB 16: Length 306:  
 Best Local Similarity 47.1% Pred. No. 25:  
 Matches 8: Conservative 3: Mismatches 6: Indels 0: Gaps 0:  
 QY 3 EKTPLTAAAXAPVXNA 19  
 DB 84 EKVPCTSSGVAPFVNA 100

RESULT 5  
 ID 09A119 PRELIMINARY: PRT: 314 AA.  
 AC 09A119:  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DE Hypoetical 34.4 kDa protein.  
 OS Escherichia coli.  
 OC Bacteria: Proteobacteria: gamma subdivision: Enterobacteriaceae:  
 NC Escherichia.  
 NCBI\_TaxID=562:  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AL62:  
 RX MEDLINE=21101044: PubMed=11159989:  
 RT Lalloué L., Le Bouguenec C.C.:  
 RT "ata-8 Gene cluster is carried by a pathogenicity island inserted into  
 RT the tRNA(Phe) of human and bovine pathogenic Escherichia coli  
 RT isolates."  
 RL Infect. Immun. 69:937-948(2001).  
 DR EMBL: AF286671; AKK7311.1; -.  
 DR HSSP: P05054; 1RK2.  
 DR InterPro: IPR002173; PfkB.  
 DR InterPro: IPR002139; Ribokinase.  
 DR Pfam: PF00294; PfkB; 1.  
 DR PRINTS: PR00990; RIBOKINSE.  
 DR Hypoetical protein.  
 KW SEQUENCE 314 AA: 34415 MW: 2D5F7342C817E3B8 CRC64:  
 SO

Query Match 54.3% Score 44: DB 2: Length 314:  
 Best Local Similarity 47.1% Pred. No. 26:  
 Matches 8: Conservative 3: Mismatches 6: Indels 0: Gaps 0:  
 QY 3 EKTPLTAAAXAPVXNA 19  
 DB 93 EKVPCTSSGVAPFVNA 109

RESULT 6  
 ID 094A00 PRELIMINARY: PRT: 427 AA.  
 AC 094A00:  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DE Hypoetical 46.8 kDa protein.  
 GN C7A10.390.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:  
 OC eurosids II: Brassicales: Brassicaceae: Arabidopsis.  
 NC NCBI\_TaxID=3702:  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,  
 RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Tortum M.,  
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,  
 RA Hayashizaki Y., Ishida J., Jones T., Kamija A., Karlin-Neumann G.,  
 RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,  
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,  
 RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,  
 RA Ecker J.R., Theologis A.:  
 RA "Full Length cDNA of gene C7A10.390 (GI:4006876).";

RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY045887; AKK76561.1; -.  
 KW Hypoetical protein.  
 SO SEQUENCE 427 AA: 46788 MW: C8B0192D3150AE41 CRC64:

Query Match 54.3% Score 44: DB 10: Length 427:  
 Best Local Similarity 60.0% Pred. No. 34:  
 Matches 9: Conservative 2: Mismatches 4: Indels 0: Gaps 0:  
 QY 2 EKTPLTAAAXAPV 16  
 DB 208 EKAEMTTAMOSPV 222

RESULT 7  
 ID 023188 PRELIMINARY: PRT: 427 AA.  
 AC 023188:  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE Hypoetical 46.8 kDa protein.  
 GN C7A10.390 OR ATG636970.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:  
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:  
 OC eurosids II: Brassicales: Brassicaceae: Arabidopsis.  
 NC NCBI\_TaxID=3702:  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Terry N., Vos P., Heljnen L., Mewes H.W., Schueller C.,  
 RA Chalwatzis N.:  
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project:  
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: Z99707: CAB16794.1; -.  
 DR EMBL: AL161590: CAB80363.1; -.  
 KW Hypoetical protein.  
 SO SEQUENCE 427 AA: 46800 MW: 75AC8E02D90AE54 CRC64:

Query Match 54.3% Score 44: DB 10: Length 427:  
 Best Local Similarity 60.0% Pred. No. 34:  
 Matches 9: Conservative 2: Mismatches 4: Indels 0: Gaps 0:  
 QY 2 EKTPLTAAAXAPV 16  
 DB 208 EKAEMTTAMOSPV 222

RESULT 8  
 ID P77924 PRELIMINARY: PRT: 506 AA.  
 AC P77924:  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Catalase isozyme.  
 GN KAT7.  
 OS Pseudomonas fluorescens.  
 OC Plasmid PAM10.6.  
 OC Bacteria: Proteobacteria: gamma subdivision: Pseudomonadaceae:  
 OC Pseudomonas.  
 NC NCBI\_TaxID=294:  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CB36:  
 RX MEDLINE=21318967: PubMed=11425481:  
 RA Peters M., Helmar A., Nurr A.:  
 RA "Plasmid-encoded catalase KAT7, the main catalase of Pseudomonas  
 RT fluorescens strain CB36.";  
 RL FEMS Microbiol. Lett. 200:235-240(2001).;

DR EMBL: U72068; AAB17009.1; -  
 DR HSSP: P43321; ZCAE.  
 DR InterPro: IPR002226; Catalase.  
 DR Pfam: PF00199; catalase; 1.  
 DR PRINTS: PR00067; CATALASE.  
 DR PRODOM: PD000510; Catalase; 1.  
 DR PROSITE: PS00438; CATALASE\_2; 1.  
 DR Plasmid.  
 KW SEQUENCE 506 AA; 57324 MW; FLEAAN78C5D4ICBE CRC64;  
 SQ  
 Query Match  
 Best Local Similarity 53.1%; Score 43; DB 2; Length 506;  
 71.4%; Pred. No. 58;  
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 TPLTTAAAPVYN 18  
 DB 11 TPLTTGAPVVDN 24  
 RESULT 9  
 Q9DWH8 PRELIMINARY; PRT: 1240 AA.

AC Q9DWH8: 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Pr2.  
 GN R2.  
 OS Rat cytomegalovirus (strain Maastricht).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Betaherpesvirinae; Murinegaleovirus.  
 OX NCBI\_Taxid=79700;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-MASTRICHT;  
 RC MEDLINE=2036325; Pubmed=10906222;  
 RA Vink C., Beuken E., Bruggeman C.A.;  
 RT "Complete DNA sequence of the rat cytomegalovirus genome";  
 RL J. Virol. 74:7656-7665 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MASTRICHT;  
 RX MEDLINE=20473137; Pubmed=11018281;  
 RA Gruithuysen Y.K., Beuken E., Bruggeman C.A.; Vink C.;  
 RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a  
 RT spliced transcript";  
 RL Virus Res. 69:119-130 (2000).  
 RN EMBL: AF232689; AAF99111.1;  
 SQ SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;  
 Query Match  
 Best Local Similarity 53.1%; Score 43; DB 12; Length 1240;  
 64.3%; Pred. No. 13e+02;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 EKTPLTTAAAPV 15  
 DB 570 EERRELTGASAPV 583

RESULT 10  
 Q9RNU2 PRELIMINARY; PRT: 210 AA.

AC Q9RNU2: 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE Serum opacity factor precursor (Fragment).  
 GN SOF4470.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Streptococcaceae; Streptococcus.  
 OX NCBI\_Taxid=1314;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=4470-96; TISSUE=BLOOD;  
 RA Beall B., Gherardi G., Lovgren M., Tyrrell G., Packham R., Forwick B.;  
 RT "Predictions of M serotype, anti-opacity factor type, and highly  
 RT related strain sets based upon the variable emm and sof gene  
 RT sequences";  
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF179217; AAD55775.1; -  
 KW Signal.  
 FT NON\_TER 1 1  
 FT SIGNAL <1 7  
 FT CHAIN 8 >210  
 FT NON\_TER 210 210  
 FT NON\_TER 210 210  
 SQ SEQUENCE 210 AA; 21220 MW; 199C89EBCF26086A CRC64;  
 Query Match  
 Best Local Similarity 51.9%; Score 42; DB 2; Length 210;  
 57.1%; Pred. No. 38;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 EKTPLTTAAAPV 15  
 DB 103 EKTPTKVTSTSPV 116  
 RESULT 11  
 Q9X6X8 PRELIMINARY; PRT: 211 AA.

AC Q9X6X8: 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE Serum opacity factor precursor (Fragment).  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Streptococcaceae; Streptococcus.  
 OX NCBI\_Taxid=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SS1401 TYPE P1658;  
 RA Beall B., Gherardi G.;  
 RT "The relation of Streptococcus pyogenes sof and emm gene sequence  
 RT types to genetically distinct strain sets";  
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF154330; AAD36988.1; -  
 KW Signal.  
 FT NON\_TER 1 1  
 FT NON\_TER <1 8  
 FT CHAIN 9 >211  
 FT NON\_TER 211 211  
 FT NON\_TER 211 211  
 SQ SEQUENCE 211 AA; 21367 MW; F5475DDC6A084FE6 CRC64;  
 Query Match  
 Best Local Similarity 51.9%; Score 42; DB 2; Length 211;  
 61.5%; Pred. No. 38;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 EKTPLTTAAAPV 14  
 DB 98 EKTPTKVTSTSPV 110

RESULT 12  
 Q9FT45 PRELIMINARY; PRT: 436 AA.

AC Q9FT45: 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE Hypothetical 48.1 kDa protein.  
 GN T25B15\_140.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI\_TaxID=3702;  
 [1]  
 SEQUENCE FROM N.A.  
 RA Alcaraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W., Rudd S.,  
 RA Lemcke K., Mayer K.F.X., Quelet F., Salanoubat M.,  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 [2]  
 SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL132972; CAC07928.1; -  
 DR InterPro: IPR000782; Bigr3\_Fasciclin.  
 DR Pfam: PF02469; Fasciclin\_1.  
 DR PROSITE: PS00976; NMT\_2; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 436 AA; 48073 MW; 83FD94879F9855DF CRC64;  
 Query Match 51.9%; Score 42; DB 10; Length 436;  
 Best Local Similarity 50.0%; Pred. No. 74;  
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 OY 2 EKKPLTTAAXAPVYXNA 19  
 DB 395 EKKPVEKTKGVYVYKKA 412  
 RESULT 13  
 O9RJK9 PRELIMINARY; PRT; 487 AA.  
 AC O9RJK9;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Catalase (EC 1.11.1.6)  
 GN KARA OR SCO0379 OR SCF62.05.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Filicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Murphy L., Harris D.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 [2]  
 SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Thompson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 [3]  
 SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Redenbach M., Kleser H.M., Denapalce D., Elchner A., Cullum J.,  
 RA Kinaschi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
 RL Mol. Microbiol. 21:77-96(1996).  
 [4]  
 SEQUENCE FROM N.A.  
 RC STRAIN-A3(2) / M145;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Collins M.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 RT coelicolor A3(2).";

Nature 417:141-147(2002).  
 CC -1- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND  
 CC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN  
 CC PEROXIDE (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) -> O(2) + 2 H(2)O.  
 DR EMBL: AL121855; CAB58320.1; -  
 DR HSSP: P42321; 2CAB.  
 DR InterPro: IPR002226; Catalase.  
 DR Pfam: PF00199; catalase; 1.  
 DR PRINTS: PR00067; CATALASE.  
 DR PRODOM: PD000510; Catalase; 1.  
 DR PROSITE: PS00437; CATALASE\_1; 1.  
 DR PROSITE: PS00438; CATALASE\_2; 1.  
 KW Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.  
 SQ SEQUENCE 487 AA; 55116 MW; 9D3334899EAF6087 CRC64;  
 Query Match 51.9%; Score 42; DB 16; Length 487;  
 Best Local Similarity 69.2%; Pred. No. 82;  
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 OY 6 PLTTAAXAPVYXN 18  
 DB 8 PLTTVAGAPVPDN 20  
 RESULT 14  
 O9SE04 PRELIMINARY; PRT; 132 AA.  
 AC O9SE04;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Copper chaperone homolog CCH.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Eriarthoidae; Oryzaeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=98369102; PubMed=9701579;  
 RA Himeblau E., Mira H., Lin S.-J., Culotta V.C., Penarrubia L.,  
 RA Amasino R.M.;  
 RT "Identification of a functional homolog of the yeast copper  
 RT homeostasis gene ATX1 from Arabidopsis.";  
 RL Plant Physiol. 117:1227-1234(1998).  
 [2]  
 SEQUENCE FROM N.A.  
 RA Mira H., Penarrubia L.;  
 RT "Copper chaperone from Oryza sativa.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF198626; AAF15285.1; -  
 DR HSSP: 000244; 1FE0.  
 DR InterPro: IPR001934; Heavy\_metal\_transpt.  
 DR Pfam: PF00403; HMA; 1.  
 SQ SEQUENCE 132 AA; 13094 MW; 7176EP95350A8231 CRC64;  
 Query Match 50.6%; Score 41; DB 10; Length 132;  
 Best Local Similarity 50.0%; Pred. No. 37;  
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 OY 2 EKKPLTTAAXAPVYXNA 19  
 DB 97 ENAPPTTAAPVYXNA 114  
 RESULT 15  
 O54272 PRELIMINARY; PRT; 417 AA.  
 AC O54272;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Hypothetical aldehyde-dehydrogenase like 43.4 kDa protein  
 DE (EC 1.2.1.-).  
 OS Streptomyces hygroscopicus.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OC NCBI\_TaxID=1912;  
 OX  
 RN  
 RP  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SF1293;  
 RX MEDLINE=95309717; PubMed=7789803;  
 RA Hidaka T., Hidaka M., Kuzuyama T., Seto H.;  
 RT "Sequence of a P-methyltransferase-encoding gene isolated from a  
 RT dialaphos-producing Streptomyces hygroscopicus.";  
 RL Gene 158:149-150(1995).  
 CC -1- PARTWAY: BIALAPHOS BIOSYNTHESIS.  
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.  
 CC EMBL: D37877; BAA07116.1; -.  
 DR HSSP: P56533; IAA5.  
 DR InterPro: IPR002086; Aldehyde\_dehydr.  
 DR pfam: PF00171; aldedh. 1.  
 DR PROSITE: PS00687; ALDEHYDE DEHYDR. GLU; UNKNOWN\_1.  
 DR Hypothetical protein: Oxidoreductase.  
 FT ACT\_SITE 187 187 BY SIMILARITY.  
 FT ACT\_SITE 221 221 BY SIMILARITY.  
 SQ SEQUENCE 417 AA; 43406 MW; 9E8714FAFB654B47 CRC64;

Query Match 50.6%; Score 41; DB 2; Length 417;  
 Best local Similarity 52.9%; Pred. No. 1e+02;  
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 3 EKTPLTTAAAPVYXNA 19  
 ||||| | | : :  
 Db 117 EKTPLTAAFAELLIEA 133

Search completed: March 14, 2003, 09:12:27  
 Job time : 33 secs